

08/560024

=> fil reg; d que stat; d 1-5 .bevreg1; fil ca, caplus; s 11
FILE 'REGISTRY' ENTERED AT 15:46:10 ON 03 APR 1997
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DICTIONARY FILE UPDATES: 1 APR 97 HIGHEST RN 187825-17-8

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seqs. 2-4

L1 5 SEA FILE=REGISTRY ABB=ON INFTRQRQPSEGSS|LFRAVITKKVAD|DVK
EADPTGHSY/SQSP

L1 ANSWER 1 OF 5 REGISTRY COPYRIGHT 1997 ACS
RN 180311-54-0 REGISTRY
CN L-Tyrosine, N-[N-[N-[N-[1-[N-[N-[N-[N2-(N-L-.alpha.-aspartyl-L-
valyl)-L-lysyl]-L-.alpha.-glutamyl]-L-alanyl]-L-.alpha.-aspartyl]-L-
prolyl]-L-threonyl]glycyl]-L-histidyl]-L-seryl]- (9CI) (CA INDEX
NAME)
SQL 12

SEQ 1 DVKEADPTGH SY
===== ==
HITS AT: 1-12

L1 ANSWER 2 OF 5 REGISTRY COPYRIGHT 1997 ACS
RN 169292-26-6 REGISTRY
CN L-Aspartic acid, N-[N-[N-[N2-[N2-[N-[N-[N-[N2-(N-L-leucyl-L-
phenylalanyl)-L-arginyl]-L-alanyl]-L-valyl]-L-isoleucyl]-L-threonyl]-
L-lysyl]-L-lysyl]-L-valyl]-L-alanyl]- (9CI) (CA INDEX NAME)
SQL 12

SEQ 1 LFRAVITKKV AD
===== ==
HITS AT: 1-12

L1 ANSWER 3 OF 5 REGISTRY COPYRIGHT 1997 ACS
RN 169292-25-5 REGISTRY
CN L-Serine, L-isoleucyl-L-asparaginyL-L-phenylalanyl-L-threonyl-L-
arginyl-L-glutaminyL-L-arginyl-L-glutaminyL-L-prolyl-L-seryl-L-
.alpha.-glutamylglycyl-L-seryl- (9CI) (CA INDEX NAME)
SQL 14

SEQ 1 INFTRQRQPS EGSS
===== ==
HITS AT: 1-14

L1 ANSWER 4 OF 5 REGISTRY COPYRIGHT 1997 ACS
RN 157298-43-6 REGISTRY
CN Antigen (human DM150 cell gene MAGE-1 reduced) (9CI) (CA INDEX
NAME)
OTHER NAMES:
CN Antigen MAGE 1 (human melanoma-associated)
CN Melanoma-assocd. antigen MAGE-1 (human cell line DM150)
Searcher : Shears 308-4994

08/560024

CN Protein (human melanoma cell line MZ2-MEL gene MAGE-1 protein)
CN Protein (human melanoma gene MAGE-1 protein)
CI MAN
SQL 309

SEQ 1 MSLEQRLHC KP EEALEAQQ EALGLVCVQA ATSSSSPLVL GTLEEVPTAG
51 STDPQPSPQG ASAFPTTINF TRQRQPSEGS SSREEEGPST SCILESIFRA
=====
101 VITKKVADLV GFLLLKYRAR EPVTKAEMLE SVIKNYKHCF PEIFGKASES
=====
151 LQLVFGIDVK EADPTGHSYV LVTCLGLSYD GLLGDNQIMP KTGFLIIVLV
=====
201 MIAMEGGHAP EEEIWEELSV MEVYDGREHS AYGEPRKLLT QDLVQEKYLE
251 YRQVPDSDPA RYEFWGPRA LAETSYVKVL EYVIKVSARV RFFFPSLREA
301 ALREEEEGV

HITS AT: 68-81, 97-108, 158-169

L1 ANSWER 5 OF 5 REGISTRY COPYRIGHT 1997 ACS
RN 146313-13-5 REGISTRY
CN Antigen (human clone B3 gene MAGE-1 reduced) (9CI) (CA INDEX NAME)
CI MAN
SQL 275

SEQ 1 MSLEQRLHC KP EEALEAQQ EALGLVCVQA ATSSSSPLVL GTLEEVPTAG
51 STDPQPSPQG ASAFPTTINF TRQRQPSEGS SSREEEGPST SCILESIFRA
=====
101 VITKKVADLV GFLLLKYRAR EPVTKAEMLE SVIKNYKHCF PEIFGKASES
=====
151 LQLVFGIDVK EADPTGHSYV LVTCLGLSYD GLLGDNQIMP KTGFLIIVLV
=====
201 MIAMEGGHAP EEEIWEELSV MEVYDREHSA YGEPRKLLTQ DLVQEKYLEY
251 GRCRTVIPHA MSSCGVQGPS LKPAM

HITS AT: 68-81, 97-108, 158-169

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L2 7 FILE CA
L3 7 FILE CAPLUS

TOTAL FOR ALL FILES
L4 14 L1

=> dup rem 14; d 1-7 .bevstr; fil hom
PROCESSING COMPLETED FOR L4
L5 7 DUP REM L4 (7 DUPLICATES REMOVED)

L5 ANSWER 1 OF 7 CA COPYRIGHT 1997 ACS DUPLICATE 1
AN 125:165697 CA
TI Monoclonal antibodies which bind to tumor rejection antigen
precursor MAGE-1 and recombinant MAGE-1 oligopeptides
Searcher : Shears 308-4994

IN Chen, Yao-tseng; Stockert, Elisabeth; Chen, Yachi; Garin-chesa, Pilar; Rettig, Wolfgang J.; Van, Der Bruggen Pierre; Boon-falleur, Thierry; Old, Lloyd J.

PA Ludwig Institute for Cancer Research, USA; Cornell Research Foundation, Inc.

SO U.S., 14 pp. Cont.-in-part of U.S. Ser. No. 37,280.
CODEN: USXXAM

PI US 5541104 A 960730

AI US 94-190411 940201

PRAI US 91-705702 910523
US 91-728838 910709
US 91-764365 910923
US 91-807043 911212
US 93-37230 930326

DT Patent

LA English

AB The invention relates to monoclonal antibodies which specifically bind to the tumor rejection antigen precursor mol. MAGE-1, hybridomas which produce these monoclonal antibodies, and their use. Also described is a recombinant form of MAGE-1, peptides which are useful as immunogens, and immunogenic compns. contg. the peptides and an adjuvant. In example, demonstrated were mol. cloning of recombinant MAGE-1 gene from human melanoma cell line MZ2-MEL 3.1, prepn. of peptides for raising monoclonal antibodies, binding of the monoclonal antibody 454 to testis lysate and MAGE-1-pos. melanomas, etc.

IT **169292-25-5P 169292-26-6P 180311-54-0P**
RL: BUU (Biological use, unclassified); SPN (Synthetic preparation); BIOL (Biological study); PREP (Preparation); USES (Uses)
(prepn. of monoclonal antibodies and recombinant peptides of tumor rejection antigen precursor MAGE-1 as immunogen)

L5 ANSWER 2 OF 7 CA COPYRIGHT 1997 ACS DUPLICATE 2

AN 123:283637 CA

TI Monoclonal antibodies which bind to tumor rejection antigen precursor MAGE-1, recombinant MAGE-1, and MAGE-1-derived immunogenic peptides

IN Chen, Yao-Tseng; Stockert, Elisabeth; Chen, Yachi; Garin-Chesa, Pilar; Rettig, Wolfgang J.; Van Der Bruggen, Pierre; Boon-Falleur, Thierry; Old, Lloyd J.

PA Ludwig Institute for Cancer Research, USA; Memorial Sloan-Kettering Cancer Center

SO PCT Int. Appl., 33 pp.
CODEN: PIXXD2

PI WO 9520974 A1 950810

DS W: AU, CA, CN, FI, JP, NO, NZ
RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE

AI WO 95-US95 950105

PRAI US 94-190411 940201

DT Patent

LA English

AB Monoclonal antibodies are provided which specifically bind to the tumor rejection antigen precursor mol. MAGE-1, as well as hybridomas which produce these monoclonal antibodies, and their use. Also described is a recombinant form of MAGE-1, peptides which are useful as immunogens, and immunogenic compns. contg. the peptides and an adjuvant.

IT **169292-25-5 169292-26-6**
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)

08/560024

(tumor rejection antigen precursor MAGE-1 fragment; monoclonal antibodies which bind to tumor rejection antigen precursor MAGE-1, recombinant MAGE-1, and MAGE-1-derived immunogenic peptides)

L5 ANSWER 3 OF 7 CA COPYRIGHT 1997 ACS DUPLICATE 3
AN 123:31227 CA
TI Cloning and characterization of the complete MAGE-1 antigen gene and immunogenicity of its peptide fragments
IN Fikes, John D.; Livingston, Brian D.; Sette, Alessandro D.; Sidney, John C.
PA Cytel Corp., USA
SO PCT Int. Appl., 57 pp.
CODEN: PIXXD2
PI WO 9504542 A1 950216
DS W: AM, AT, AU, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, ES, FI, GB, GE, HU, JP, KE, KG, KP, KR, KZ, LK, LT, LU, LV, MD, MG, MN, MW, NL, NO, NZ, PL, PT, RO, RU, SD, SE, SI, SK, TJ, TT, UA, US, UZ, VN
RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, DE, DK, ES, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG
AI WO 94-US8721 940802
PRAI US 93-103623 930806
DT Patent
LA English
AB The complete nucleotide and amino acid sequences of the human MAGE-1 antigen are provided. Peptides from residues of the C-terminal are used to define epitopes that stimulate HLA-restricted cytotoxic T lymphocyte activity against MAGE-1 antigens. The peptides are particularly useful in methods for stimulating the immune response of individuals against MAGE-1 antigens assocd. with melanomas.
IT **157298-43-6P**
RL: BAC (Biological activity or effector, except adverse); BPN (Biosynthetic preparation); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(amino acid sequence; cloning and characterization of human MAGE-1 antigen gene and immunogenicity of its peptide fragments)

L5 ANSWER 4 OF 7 CA COPYRIGHT 1997 ACS DUPLICATE 4
AN 121:278375 CA
TI Autologous cytolytic T lymphocytes recognize a MAGE-1 nonapeptide on melanomas expressing HLA-Cw*1601*
AU van der Bruggen, Pierre; Szikora, Jean-Pierre; Boeel, Pascale; Wildmann, Claude; Somville, Michel; Sensi, Marialuisa; Boon, Thierry
CS Ludwig Inst. Cancer Res., Cellular Genetics Unit, Univ. Catholique de Louvain, Belg.
SO Eur. J. Immunol. (1994), 24(9), 2134-40
CODEN: EJIMAF; ISSN: 0014-2980
DT Journal
LA English
AB Human melanoma cell line MZ2-MEL expresses several antigens recognized by autologous cytolytic T lymphocyte (CTL) clones. We reported previously the identification of a gene, named MAGE-1, which codes for antigen MZ2-E which is presented by HLA-A1. Gene MAGE-1 is expressed in many tumors of several types but not in normal tissues except for testis. We show here that gene MAGE-1 directs the expression of another antigen recognized by CTL on the MZ2-MEL cells. This antigen, which was named MZ2-Bb, consists of MAGE-1-encoded peptide SAYGEPRKL bound to major histocompatibility mol. HLA-Cw*1601. The HLA-Cw*1601 allele was found to be expressed
Searcher : Shears 308-4994

*published
Sept 94
pc*

by 7 out of 99 individuals from a Caucasian population. Our results extend the range of tumor patients who could be eligible for immunization against MAGE antigens.

IT **157298-43-6**

RL: PRP (Properties)

(autologous cytolytic T lymphocytes recognize a MAGE-1 nonapeptide on melanomas expressing HLA-Cw*1601*)

L5 ANSWER 5 OF 7 CA COPYRIGHT 1997 ACS

DUPLICATE 5

AN 122:103468 CA

TI Identification of potential CTL epitopes of tumor-associated antigen MAGE-1 for five common HLA-A alleles

AU Celis, Esteban; Fikes, John; Wentworth, Peggy; Sidney, John; Southwood, Scott; Maewal, Ajesh; Del Guercio, Marie-France; Sette, Alessandro; Livingston, Brian

CS Cytel Corporation, San Diego, CA, 92121, USA

SO Mol. Immunol. (1994), 31(18), 1423-30

CODEN: MOIMD5; ISSN: 0161-5890

DT Journal

LA English

AB Identification of CTL epitopes for tumor-specific responses is important for the development of immunotherapies to treat cancer patients. We have developed a strategy to identify potential CTL epitopes based on screening of sequences of target proteins for presence of specific motifs recognized by the most common HLA-A alleles, and identification of high affinity binding peptides using in vitro quant. assays. A systematic anal. using the sequence of the product of the tumor-assocd. MAGE-1 gene has been carried out. All possible peptides of nine and ten residues, contg. binding motifs for HLA-A1, -A2.1, A-3.2, -A11 and -A24 were synthesized and tested for binding using a quant. assay. Out of 237 possible peptide/MHC combinations, 47 cases demonstrated good binding affinity (Kd .ltoreq. 500 nM). Several peptides were identified as good MHC binders for each one of the five HLA-A alleles studied (five for HLA-A1, 11 for HLA-A2.1, 10 for HLA-A3.2, 16 for HLA-A11 and five for HLA-A24). Furthermore, eight of these peptides were found to bind well to more than one HLA-A allele. These results have important implications for the development of immunotherapeutic vaccines to treat malignant melanoma.

IT **157298-43-6**

RL: PRP (Properties)

(potential melanoma-specific CTL epitopes of tumor-assocd. antigen MAGE-1 for five common HLA-A alleles)

L5 ANSWER 6 OF 7 CA COPYRIGHT 1997 ACS

DUPLICATE 6

AN 121:155075 CA

TI Cloning and analysis of MAGE-1-related genes

AU Ding, Min; Beck, Raymond J.; Keller, Christopher J.; Fenton, Robert G.

CS Clinical Research Branch, NCI, Frederick, MD, 21702, USA

SO Biochem. Biophys. Res. Commun. (1994), 202(1), 549-55

CODEN: BBRCA9; ISSN: 0006-291X

DT Journal

LA English

AB The spectrum of MAGE gene expression in the human melanoma cell line DM150 was examd. using reverse transcription polymerase chain reaction and cDNA cloning. Five full-length cDNAs were isolated from DM150 which were identified as MAGE-1, MAGE-3, MAGE-12, and 2 previously undescribed MAGE genes, MAGE-3b and MAGE-X2. DNA sequence anal. of the coding regions of the MAGE-3b and MAGE-X2

Searcher : Shears 308-4994

*published
12/94
P*

*published
7/94
P*

genes revealed 83 and 88% identity with MAGE-1, whereas MAGE-3b was 98% homologous with the full-length MAGE-3 clone. The predicted amino acid sequences of MAGE-X2 and MAGE-3b contain consensus HLA-A1 peptide binding motifs, suggesting that, like MAGE 1, they may code for tumor-assocd. antigens. In addn., a nonamer peptide encoded by both the MAGE-3 and MAGE-12 genes was shown by direct binding studies to contain an aggretope for HLA-A2.

IT **157298-43-6**, Melanoma-assocd. antigen MAGE-1 (human cell line DM150)

RL: BIOL (Biological study)

(amino acid sequence and aggretope moieties of)

L5 ANSWER 7 OF 7 CA COPYRIGHT 1997 ACS

DUPLICATE 7

AN 118:121916 CA

TI A gene encoding an antigen recognized by cytolytic T lymphocytes on a human melanoma

AU Van der Bruggen, P.; Traversari, C.; Chomez, P.; Lurquin, C.; De Plaen, E.; Van den Eynde, B.; Knuth, A.; Boon, T.

CS Ludwig Inst. Cancer Res., Brussels, B-1200, Belg.

SO Science (Washington, D. C., 1883-) (1991), 254(5038), 1643-7

CODEN: SCIEAS; ISSN: 0036-8075

DT Journal

LA English

AB Many human melanoma tumors express antigens that are recognized in vitro by cytolytic T lymphocytes (CTLs) derived from the tumor-bearing patient. A gene was identified that directed the expression of antigen MZ2-E on a human melanoma cell line. This gene shows no similarity to known sequences and belongs to a family of at least three genes. It is expressed by the original melanoma cells, other melanoma cell lines, and by some tumor cells of other histol. types. No expression was obsd. in a panel of normal tissues. Antigen MZ2-E appears to be presented by HLA-A1; anti-MZ2-E CTLs of the original patient recognized two melanoma cell lines of other HLA-A1 patients that expressed the gene. Thus, precisely targeted immunotherapy directed against antigen MZ2-E could be provided to individuals identified by HLA typing and anal. of the RNA of a small tumor sample.

IT **146313-13-5**, Antigen (human clone B3 gene MAGE-1 reduced)

RL: PRP (Properties)

(amino acid sequence of, complete)

FILE 'HOME' ENTERED AT 15:46:29 ON 03 APR 1997

\$%^Other;HighlightOn=**,HighlightOff=**;
Trying 01083...Open

=> s MAGE-I

175 MAGE
2267795 I
L1 33 MAGE-I
(MAGE(W)I)

=> d I1 1-33

1. 5,736,142, Apr. 7, 1998, Alteration of immune response using pan DR-binding peptides; Alessandro Sette, et al., 424/185.1, 184.1, 193.1; 514/2, 15; 530/300, 327, 332, 868 [IMAGE AVAILABLE]
2. 5,712,307, Jan. 27, 1998, Methods of inducing the production of hemoglobin and treating pathologies associated with abnormal hemoglobin activity using phenylacetic acids and derivatives thereof; Dvorit Samid, 514/538, 563, 567 [IMAGE AVAILABLE]
3. 5,710,178, Jan. 20, 1998, Compositions and methods for therapy and prevention of pathologies including cancer, AIDS, and anemia; Dvorit Samid, 514/557, 568, 570 [IMAGE AVAILABLE]
4. 5,708,025, Jan. 13, 1998, Methods for promoting wound healing; Dvorit Samid, 514/538, 563, 567, 885, 886, 928 [IMAGE AVAILABLE]
5. 5,698,396, Dec. 16, 1997, Method for identifying auto-immunoreactive substances from a subject; Michael Pfreundschuh, 435/6, 5, 7.1, 7.23 [IMAGE AVAILABLE]
6. 5,695,994, Dec. 9, 1997, Isolated cytolytic T cells specific for complexes of MAGE related peptides and HLA molecules; Thierry Boon-Falleur, et al., 435/325, 355, 372.3; 530/328 [IMAGE AVAILABLE]
7. 5,686,068, Nov. 11, 1997, Isolated peptides derived from MAGE-2, cytolytic T cells specific to complexes of peptide and HLA-A2 molecules, and uses thereof; Cornelius J. M. Melief, et al., 424/93.71, 185.1, 277.1; 435/7.23; 530/328, 828 [IMAGE AVAILABLE]
8. 5,683,886, Nov. 4, 1997, Tumor rejection antigens which correspond to amino acid sequences in tumor rejection antigen precursor bage, and uses thereof; Pierre van der Bruggen, et al., 435/7.24; 424/93.71, 277.1; 435/7.1, 7.23; 530/324, 325, 326, 327, 328, 329, 330 [IMAGE AVAILABLE]
9. 5,674,749, Oct. 7, 1997, Monoclonal antibodies which bind to tumor rejection antigen precursor melan-A, and uses thereof; Yao-tseng Chen, et al., 435/344.1; 530/388.1, 388.85 [IMAGE AVAILABLE]
10. 5,662,907, Sep. 2, 1997, Induction of anti-tumor cytotoxic T lymphocytes in humans using synthetic peptide epitopes; Ralph T. Kubo, et al., 424/195.1, 193.1, 197.11, 277.1; 530/300, 328, 403 [IMAGE AVAILABLE]
11. 5,661,179, Aug. 26, 1997, Methods for treating neoplastic conditions using phenylacetic acid and derivatives thereof; Dvorit Samid, 514/538, 563, 567; 560/19 [IMAGE AVAILABLE]
12. 5,654,333, Aug. 5, 1997, Methods for prevention of cancer using phenylacetic acids and derivatives thereof; Dvorit Samid, 514/538, 563, 567 [IMAGE AVAILABLE]
13. 5,648,226, Jul. 15, 1997, Isolated peptides derived from tumor rejection antigens, and their use; Benoit Van den Eynde, et al., 435/7.24; 424/185.1, 277.1; 435/7.23; 530/326, 327, 328, 828 [IMAGE AVAILABLE]
14. 5,635,533, Jun. 3, 1997, Methods for inducing differentiation of a cell using phenylacetic acid and derivatives; Dvorit Samid, 514/538, 563, 567 [IMAGE AVAILABLE]
15. 5,635,532, Jun. 3, 1997, Compositions and methods for therapy and prevention of pathologies including cancer, AIDS and anemia; Dvorit Samid, 514/538, 563, 567; 560/19 [IMAGE AVAILABLE]
16. 5,629,166, May 13, 1997, Method for identifying individuals suffering from a cellular abnormality some of whose abnormal cells present complexes of HLA-C-clone 10/**MAGE**.*1** derived peptides, and methods for treating said individuals; Pierre van der Bruggen, et al., 435/7.23, 6, 7.21; 436/64 [IMAGE AVAILABLE]
17. 5,620,886, Apr. 15, 1997, Isolated nucleic acid sequence coding for a tumor rejection antigen precursor processed to at least one tumor rejection antigen presented by HLA-A2; Vincent Brichard, et al., 435/325, 7.23, 29, 252.3, 320.1; 514/44; 530/350; 536/22.1, 23.1, 23.5 [IMAGE AVAILABLE]

18. 5,612,201, Mar. 18, 1997, Isolated nucleic acid molecules useful in determining expression of a tumor rejection antigen precursor; Etienne De Plaen, et al., 435/91.2, 6; 536/23.1, 24.33 [IMAGE AVAILABLE]
19. 5,610,013, Mar. 11, 1997, Method for diagnosing a disorder by determining expression of gage tumor rejection antigen precursors; Benoit Van den Eynde, et al., 435/6, 7.1, 252.3, 252.33, 320.1, 325, 358, 362, 365; 536/23.5 [IMAGE AVAILABLE]
20. 5,605,930, Feb. 25, 1997, Compositions and methods for treating and preventing pathologies including cancer; Dvorit Samid, 514/510, 513, 515, 529, 538, 563, 567 [IMAGE AVAILABLE]
21. 5,591,430, Jan. 7, 1997, Isolated, MAGE-3 derived peptides which complex with HLA-A2 molecules and uses thereof; Alan Townsend, et al., 424/93.71, 185.1, 277.1; 435/7.24, 372.3; 530/328, 395, 828 [IMAGE AVAILABLE]
22. 5,587,289, Dec. 24, 1996, Isolated nucleic acid molecules which are members of the MAGE-Xp family and uses thereof; Christophe Lurquin, et al., 435/6, 252.3, 320.1, 325; 536/23.1 [IMAGE AVAILABLE]
23. 5,585,461, Dec. 17, 1996, Isolated, MAGE-3 derived peptides which complex with HLA-A2 molecules and uses thereof; Alan Townsend, et al., 530/328; 424/185.1; 530/300, 395, 865 [IMAGE AVAILABLE]
24. 5,571,711, Nov. 5, 1996, Isolated nucleic acid molecules coding for BAGE tumor rejection antigen precursors; Pierre van der Bruggen, et al., 435/365, 69.3, 172.3, 252.3, 320.1; 536/23.5; 935/9, 32, 34, 55, 57, 70, 71 [IMAGE AVAILABLE]
25. 5,558,995, Sep. 24, 1996, Peptides which are derived from tumor rejection antigen precursor molecule **MAGE**.*1**, which complex to MHC molecule HLA-C clone 10, and uses thereof; Pierre van der Bruggen, et al., 435/7.24; 424/185.1, 277.1; 435/372.3; 530/326, 327, 328, 828 [IMAGE AVAILABLE]
26. 5,554,724, Sep. 10, 1996, Isolated tumor rejection antigen precursor MAGE-2 derived peptides, and uses thereof; Cornelis J. M. Melief, et al., 530/328; 424/185.1, 277.1; 530/300, 327, 828 [IMAGE AVAILABLE]
27. 5,554,506, Sep. 10, 1996, Isolated, MAGE-3 derived peptides which complex with HLA-A2 molecules and uses thereof; Pierre van der Bruggen, et al., 435/7.24; 424/185.1, 193.1, 273.1; 435/372.3; 514/2, 15; 530/300, 328, 828 [IMAGE AVAILABLE]
28. 5,541,104, Jul. 30, 1996, Monoclonal antibodies which bind to tumor rejection antigen precursor **mage**.*1**; Yao-Tseng Chen, et al., 435/344.1; 424/138.1, 155.1, 174.1; 435/69.6, 70.21, 172.2; 530/350, 387.7, 388.8; 935/15 [IMAGE AVAILABLE]
29. 5,512,444, Apr. 30, 1996, Method for determining bladder tumors by assaying for MAGE-1,2,3 or 4; Jean-Jacques Patard, et al., 435/6, 7.1, 7.9, 91.2; 536/23.1, 24.3 [IMAGE AVAILABLE]
30. 5,512,437, Apr. 30, 1996, Method for determining head and neck squamous cell carcinomas, prostate carcinomas, and bladder tumors by assaying for mage-3; Beatrice Gaugler, et al., 435/6, 7.1, 7.9, 91.2; 536/23.1, 24.3 [IMAGE AVAILABLE]
31. 5,462,871, Oct. 31, 1995, Isolated nucleic acid molecules which encode MAGE derived nonapeptides; Thierry Boon-Falleur, et al., 435/354, 252.3, 365; 536/23.1, 23.5 [IMAGE AVAILABLE]
32. 5,405,940, Apr. 11, 1995, Isolated nonapeptides derived from MAGE genes and uses thereof; Thierry Boon, et al., 530/328; 424/185.1; 530/300 [IMAGE AVAILABLE]
33. 5,342,774, Aug. 30, 1994, Nucleotide sequence encoding the tumor rejection antigen precursor, **MAGE**.*1**; Thierry Boon, et al., 435/371, 69.1, 69.3, 172.3, 235.1, 252.3, 320.1; 530/350; 536/23.5; 935/9, 32, 34, 57, 62, 70, 71 [IMAGE AVAILABLE]

08/560024

=> fil ca,caplus
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=> s mage(w) (1 or i)
L1 94 FILE CA
L2 97 FILE CAPLUS

-key terms

TOTAL FOR ALL FILES
L3 191 MAGE(W) (1 OR I)

=> s magei or mage1
L4 34 FILE CA
L5 35 FILE CAPLUS

TOTAL FOR ALL FILES
L6 69 MAGEI OR MAGE1

=> s (l3 or l6) (l) (polypeptide# or polyprotein# or protein# or peptide# or antigen#)
L7 94 FILE CA
L8 97 FILE CAPLUS

TOTAL FOR ALL FILES
L9 191 (L3 OR L6) (L) (POLYPEPTIDE# OR POLYPROTEIN# OR PROTEIN# OR PEPTIDE# OR ANTIGEN#)

=> s (l3 or l6) (l) antigen#
L10 90 FILE CA
L11 92 FILE CAPLUS

TOTAL FOR ALL FILES
L12 182 (L3 OR L6) (L) ANTIGEN#

=> s l12(l) (polypeptide# or polyprotein# or protein# or peptide#)
L13 49 FILE CA
L14 51 FILE CAPLUS

TOTAL FOR ALL FILES
L15 100 L12(L) (POLYPEPTIDE# OR POLYPROTEIN# OR PROTEIN# OR PEPTIDE#)

=> s l15 and (moab# or mab# or monoclon? or hybridom?)
L16 7 FILE CA
L17 7 FILE CAPLUS

TOTAL FOR ALL FILES
L18 14 L15 AND (MOAB# OR MAB# OR MONOCLON? OR HYBRIDOM?)

=> s l9 and (moab# or mab# or monoclon? or hybridom?)
L19 10 FILE CA
L20 10 FILE CAPLUS

TOTAL FOR ALL FILES
L21 20 L9 AND (MOAB# OR MAB# OR MONOCLON? OR HYBRIDOM?)

08/560024

=> s 118 or 121

L22 10 FILE CA

L23 10 FILE CAPLUS

TOTAL FOR ALL FILES

L24 20 L18 OR L21

=> dup rem 124

PROCESSING COMPLETED FOR L24

L25 10 DUP REM L24 (10 DUPLICATES REMOVED)

=> d 1-10 .bevstr1; fil

biosi,medl,embas,lifesci,biotechd,wpid,confsci,dissabs,scisearch,jicst,cancerlit

L25 ANSWER 1 OF 10 CA COPYRIGHT 1997 ACS DUPLICATE 1

AN 125:165697 CA

TI **Monoclonal** antibodies which bind to tumor rejection

antigen precursor **MAGE-1** and recombinant

MAGE-1 oligopeptides

IN Chen, Yao-tseng; Stockert, Elisabeth; Chen, Yachi; Garin-chesa,
Pilar; Rettig, Wolfgang J.; Van, Der Bruggen Pierre; Boon-falleur,
Thierry; Old, Lloyd J.

PA Ludwig Institute for Cancer Research, USA; Cornell Research
Foundation, Inc.

SO U.S., 14 pp. Cont.-in-part of U.S. Ser. No. 37,280.
CODEN: USXXAM

PI US 5541104 A 960730

AI US 94-190411 940201

PRAI US 91-705702 910523

US 91-728838 910709

US 91-764365 910923

US 91-807043 911212

US 93-37230 930326

DT Patent

LA English

AB The invention relates to **monoclonal** antibodies which
specifically bind to the tumor rejection **antigen** precursor
mol. **MAGE-1**, **hybridomas** which produce
these **monoclonal** antibodies, and their use. Also
described is a recombinant form of **MAGE-1**,
peptides which are useful as immunogens, and immunogenic
compns. contg. the **peptides** and an adjuvant. In example,
demonstrated were mol. cloning of recombinant **MAGE-**
1 gene from human melanoma cell line MZ2-MEL 3.1, prepn. of
peptides for raising **monoclonal** antibodies,
binding of the **monoclonal** antibody 454 to testis lysate
and **MAGE-1**-pos. melanomas, etc.

IT **Antigens**

RL: BUU (Biological use, unclassified); SPN (Synthetic preparation);

BIOL (Biological study); PREP (Preparation); USES (Uses)

(**MAGE-1** gene **peptide**; prepn. of

monoclonal antibodies and recombinant **peptides**

of tumor rejection **antigen** precursor **MAGE-**

1 as immunogen)

IT Gene, animal

RL: BPN (Biosynthetic preparation); BSU (Biological study,
unclassified); BIOL (Biological study); PREP (Preparation)

(**MAGE-1**; prepn. of **monoclonal**

antibodies and recombinant **peptides** of tumor rejection

antigen precursor **MAGE-1** as

Searcher : Shears 308-4994

- immunogen)
- IT **Antigens**
 RL: PRP (Properties)
 (MAGE-1; prepn. of **monoclonal** antibodies and recombinant **peptides** of tumor rejection **antigen** precursor MAGE-1 as immunogen)
- IT Animal cell line
 (MZ2-MEL3.1; prepn. of **monoclonal** antibodies and recombinant **peptides** of tumor rejection **antigen** precursor MAGE-1 as immunogen)
- IT Melanoma
 (cell lines; prepn. of **monoclonal** antibodies and recombinant **peptides** of tumor rejection **antigen** precursor MAGE-1 as immunogen)
- IT Deoxyribonucleic acid sequences
Protein sequences
 Testis
 (prepn. of **monoclonal** antibodies and recombinant **peptides** of tumor rejection **antigen** precursor MAGE-1 as immunogen)
- IT **Antigens**
 RL: BSU (Biological study, unclassified); BIOL (Biological study)
 (TRA (tumor-rejection **antigen**), precursor MAGE-1; prepn. of **monoclonal** antibodies and recombinant **peptides** of tumor rejection **antigen** precursor MAGE-1 as immunogen)
- IT Antibodies
 RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
 (**monoclonal**, prepn. of **monoclonal** antibodies and recombinant **peptides** of tumor rejection **antigen** precursor MAGE-1 as immunogen)
- IT 180473-66-9
 RL: PRP (Properties)
 (nucleotide sequence; prepn. of **monoclonal** antibodies and recombinant **peptides** of tumor rejection **antigen** precursor MAGE-1 as immunogen)
- IT 169292-25-5P 169292-26-6P 180311-54-0P
 RL: BUU (Biological use, unclassified); SPN (Synthetic preparation); BIOL (Biological study); PREP (Preparation); USES (Uses)
 (prepn. of **monoclonal** antibodies and recombinant **peptides** of tumor rejection **antigen** precursor MAGE-1 as immunogen)

L25 ANSWER 2 OF 10 CA COPYRIGHT 1997 ACS DUPLICATE 2
 AN 125:192240 CA
 TI **Monoclonal** antibodies against recombinant MAGE-1 **protein** identify a cross-reacting 72-kDa **antigen** which is co-expressed with MAGE-1 **protein** in melanoma cells
 AU Carrel, Stefan; Schreyer, Magali; Spagnoli, Giulio; Cerottini, Jean-Charles; Rimoldi, Donata
 CS Ludwig Institute Cancer Research, University Lausanne, Epalinges, 1066, Switz.
 SO Int. J. Cancer (1996), 67(3), 417-422
 CODEN: IJCNAA; ISSN: 0020-7136
 DT Journal

LA English

AB The **MAGE-1** gene codes for tumor-assocd. **peptides** recognized by cytolytic T lymphocytes in assocn. with MHC class I mols. such as HLA-A1 and HLA-Cw16. In the course of a study aimed at the immunohistochem. detection of the **MAGE-1** gene product in tumor samples, 2 mouse **monoclonal** antibodies (**MABs**) directed against a full-length recombinant **MAGE-1** fusion **protein** were found to react strongly not only with the 46-kDa **MAGE-1 protein**, but also with a 72-kDa product in immunoblots of lysates obtained from several **MAGE-1**-mRNA-pos. melanoma cell lines. Pre-incubation of the antibodies with the recombinant **MAGE-1** fusion **protein** abolished their reactivity both with **MAGE-1 protein** and with the 72-kDa product, thus confirming the occurrence of antigenic determinant(s) shared by the 2 **proteins**. The 72-kDa **protein** is not an alternative product of **MAGE-1**, since it was still detected in lysates of a **MAGE-1** loss variant derived from a **MAGE-1**-pos. melanoma cell line. Moreover, the 72-kDa **protein** does not appear to be a product of the other members of the **MAGE** gene family known to be expressed in tumors (such as **MAGE-2**, **-3**, **-4** and **-12**). Interestingly, expression of the 72-kDa **protein** was correlated with that of **MAGE-1 protein**. Thus, in 30 tumor cell lines analyzed by immunoblotting and RT-PCR, the 72-kDa **protein** was never detected in **MAGE-1**-mRNA-neg. cell lines, while it was co-expressed with **MAGE-1 protein** in 12 out of 15 cell lines expressing **MAGE-1**. Furthermore, the 72-kDa **protein** was detected in lysates of human testis, the only normal tissue known to express **MAGE-1**. Finally, treatment of **MAGE-1**-mRNA-neg. cell lines with 5-aza-2'-deoxycytidine, a hypomethylating agent known to induce **MAGE-1** expression, resulted in the expression of the 72-kDa **protein**. Taken collectively, these findings suggest that expression of the gene encoding the 72-kDa **protein** identified in this study through antigenic determinant(s) shared with **MAGE-1 protein** is regulated in a way similar to that of **MAGE-1**.

IT **Antigens**

RL: BPR (Biological process); BIOL (Biological study); PROC (Process)

(**MAGE-1**; **monoclonal** antibodies to **MAGE-1** cross-react with 72 kDa **protein** in melanoma cells)

IT Testis

(**monoclonal** antibodies to **MAGE-1** cross-react with 72 kDa **protein** in)

IT Melanoma

(**monoclonal** antibodies to **MAGE-1** cross-react with 72 kDa **protein** in melanoma cells)

IT **Proteins**, specific or class

RL: BOC (Biological occurrence); BPR (Biological process); MFM (Metabolic formation); PRP (Properties); BIOL (Biological study); FORM (Formation, nonpreparative); OCCU (Occurrence); PROC (Process)
(72,000-mol.-wt., **monoclonal** antibodies to **MAGE-1** cross-react with 72 kDa **protein** in melanoma cells)

IT Antibodies
 RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
 (monoclonal, monoclonal antibodies to **MAGE-1** cross-react with 72 kDa **protein** in melanoma cells)

L25 ANSWER 3 OF 10 CA COPYRIGHT 1997 ACS DUPLICATE 3
 AN 126:155770 CA
 TI The tumor-associated **antigen MAGE-1** is detectable in formalin-fixed paraffin sections of malignant melanoma
 AU Gudat, F.; Zuber, M.; Duermueller, U.; Kocher, T.; Schaefer, C.; Noppen, C.; Spagnoli, G.
 CS Institute Pathology, University Basel, Basel, CH-4003, Switz.
 SO Virchows Arch. (1996), 429(2/3), 77-81
 CODEN: VARCEM; ISSN: 0945-6317
 DT Journal
 LA English
 AB It was studied the detection of **MAGE-1 protein** by immunohistochem. on native and formalin-fixed, paraffin-embedded melanoma biopsies. Native, frozen tissues from the same tumors were used to validate the results. Of 4 **monoclonal** antibodies tested (AB), **mAB 34B** and **mAB 77B** were highly efficient in detecting **MAGE-1 protein** in deparafinized sections with the regular Avidin-Biotin complex method after microwave treatment. In 28 addnl. primary biopsies embedded in paraffin 75% expressed **MAGE-1**, 50% in a substantial proportion. Follow-up biopsies in 6 patients until 16 mo indicate that the expression pattern remains stable but may change substantially in a short range.

IT Tumor-associated **antigen**
 RL: BOC (Biological occurrence); BIOL (Biological study); OCCU (Occurrence)
 (**MAGE-1**; the tumor-assocd. **antigen MAGE-1** is detectable in formalin-fixed paraffin sections of malignant melanoma)

IT Melanoma
 (the tumor-assocd. **antigen MAGE-1** is detectable in formalin-fixed paraffin sections of malignant melanoma)

IT Monoclonal antibodies
 RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
 (the tumor-assocd. **antigen MAGE-1** is detectable in formalin-fixed paraffin sections of malignant melanoma)

L25 ANSWER 4 OF 10 CA COPYRIGHT 1997 ACS DUPLICATE 4
 AN 123:283637 CA
 TI **Monoclonal** antibodies which bind to tumor rejection **antigen** precursor **MAGE-1**, recombinant **MAGE-1**, and **MAGE-1**-derived immunogenic **peptides**
 IN Chen, Yao-Tseng; Stockert, Elisabeth; Chen, Yachi; Garin-Chesa, Pilar; Rettig, Wolfgang J.; Van Der Bruggen, Pierre; Boon-Falleur, Thierry; Old, Lloyd J.
 PA Ludwig Institute for Cancer Research, USA; Memorial Sloan-Kettering Cancer Center
 SO PCT Int. Appl., 33 pp.

CODEN: PIXXD2

PI WO 9520974 A1 950810
 DS W: AU, CA, CN, FI, JP, NO, NZ
 RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE
 AI WO 95-US95 950105
 PRAI US 94-190411 940201
 DT Patent
 LA English
 AB **Monoclonal** antibodies are provided which specifically bind to the tumor rejection **antigen** precursor mol. **MAGE-1**, as well as **hybridomas** which produce these **monoclonal** antibodies, and their use. Also described is a recombinant form of **MAGE-1**, **peptides** which are useful as immunogens, and immunogenic compns. contg. the **peptides** and an adjuvant.
 IT **Antigens**
 RL: BPN (Biosynthetic preparation); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); PREP (Preparation); USES (Uses)
 (**MAGE-1**; **monoclonal** antibodies which bind to tumor rejection **antigen** precursor **MAGE-1**, recombinant **MAGE-1**, and **MAGE-1**-derived immunogenic **peptides**)
 IT **Hybridoma**
 Immunoassay
 (**monoclonal** antibodies which bind to tumor rejection **antigen** precursor **MAGE-1**, recombinant **MAGE-1**, and **MAGE-1**-derived immunogenic **peptides**)
 IT **Protein** sequences
 (of tumor rejection **antigen** precursor **MAGE-1** from human)
 IT Deoxyribonucleic acid sequences
 (complementary, for tumor rejection **antigen** precursor **MAGE-1** from human)
 IT **Antibodies**
 RL: BPN (Biosynthetic preparation); BUU (Biological use, unclassified); BIOL (Biological study); PREP (Preparation); USES (Uses)
 (**monoclonal**, MA454; **monoclonal** antibodies which bind to tumor rejection **antigen** precursor **MAGE-1**, recombinant **MAGE-1**, and **MAGE-1**-derived immunogenic **peptides**)
 IT 169440-60-2P
 RL: BPN (Biosynthetic preparation); PRP (Properties); BIOL (Biological study); PREP (Preparation)
 (nucleotide sequence; **monoclonal** antibodies which bind to tumor rejection **antigen** precursor **MAGE-1**, recombinant **MAGE-1**, and **MAGE-1**-derived immunogenic **peptides**)
 IT 169292-25-5 169292-26-6 169292-27-7
 RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
 (tumor rejection **antigen** precursor **MAGE-1** fragment; **monoclonal** antibodies which bind to tumor rejection **antigen** precursor **MAGE-1**, recombinant **MAGE-1**, and **MAGE-1**-derived immunogenic **peptides**)

L25 ANSWER 5 OF 10 CA COPYRIGHT 1997 ACS DUPLICATE 5
 AN 123:6907 CA
 TI Identification and intracellular location of MAGE-3 gene product
 AU Kocher, Thomas; Schultz-Thater, Elke; Gudat, Fred; Schaefer, Christoph; Casorati, Giulia; Juretic, Antonio; Willimann, Thomas; Harder, Felix; Heberer, Michael; Spagnoli, Giulio C.
 CS Dep. Surgery Res., Univ. Basel, Basel, Switz.
 SO Cancer Res. (1995), 55(11), 2236-9
 CODEN: CNREA8; ISSN: 0008-5472
 DT Journal
 LA English
 AB The human MAGE-3 gene encodes a melanoma antigenic epitope recognized by specific cytotoxic T lymphocytes, but its gene product has not been identified thus far. The authors produced a recombinant MAGE-3 gene product by expression cloning of the entire reading frame in the context of a fusion **protein** characterized by a 10-histidine tail, allowing purifn. by metal chelation on a nickel Sepharose column. The semi-purified product was used to generate MAGE-3-specific **monoclonal** antibodies. One reagent could identify by immunoblotting the native MAGE-3 gene product as a Mr 48,000 **protein** in lysates of cell lines showing evidence of MAGE-3 gene expression. No apparent cross-reactivity with recombinant or native **MAGE-1** gene product was obsd. Immunohistochem. shows that, closely resembling the **MAGE-1** gene product, MAGE-3 is a cytoplasmic **protein**.
 IT Gene, animal
 RL: BSU (Biological study, unclassified); BIOL (Biological study) (MAGE-3; identification and intracellular location of human MAGE-3 gene product)
 IT Antigens
 RL: BOC (Biological occurrence); PRP (Properties); BIOL (Biological study); OCCU (Occurrence) (gene MAGE-3; identification and intracellular location of human MAGE-3 gene product)
 IT Cytoplasm
 Melanoma (identification and intracellular location of human MAGE-3 gene product)

L25 ANSWER 6 OF 10 CA COPYRIGHT 1997 ACS DUPLICATE 6
 AN 124:25111 CA
 TI Establishment of an enzyme-linked immunosorbent assay (ELISA) for measuring cellular MAGE-4 protein on human cancers
 AU Shichijo, Shigeki; Tsunosue, Rika; Kubo, Keisuke; Kuramoto, Terukazu; Tanaka, Yasuyuki; Hayashi, Akihiko; Itoh, Kyogo
 CS Department of Immunology, Kurume University School of Medicine, Kurume, Japan
 SO J. Immunol. Methods (1995), 186(1), 137-49
 CODEN: JIMMBG; ISSN: 0022-1759
 DT Journal
 LA English
 AB The MAGE genes encoding tumor-rejection **antigens** are expressed on various human cancers. An ELISA (ELISA) was established for measuring cellular MAGE-4 **protein** (MAGE-4a and/or -4b) expressed on human tumor cells using a **monoclonal** antibody (**mAb**) and polyclonal Ab to recombinant MAGE-4b **protein**. Both the R5 **mAb** (IgG1) and the polyclonal Ab recognized a 45 kDa **protein**
 Searcher : Shears 308-4994

in exts. of MAGE-4 mRNA pos. cancers, and showed no apparent cross-reactivity to the other MAGE gene products (MAGE-1, -2, -3, -6, and -12) by the immunoblot analyses. The R5 mAb and the polyclonal Ab primarily recognized one (the position 119-133) and two oligopeptides (the positions 119-133 and 259-273), resp., among a series of 31 different MAGE-4b oligopeptides. The amino acid sequences of these two peptides were identical to those of MAGE-4a and -4b, but differed from those of all the other MAGE proteins (MAGE-1, -2, -3, -6, and -12). Substitution of glycine for amino acid in position 123 (arginine, R), 124 (lysine, K), 126 (R) or 128 (K) in a MAGE-4b oligopeptide of the position 119-132 severely decreased the reactivity of the R5 mAb to the oligopeptide. This ELISA also showed no apparent cross-reactivity with the other MAGE gene products (MAGE-1, -2, -3, -6, and -12). The min. detectable level of MAGE-4 protein was detd. to be 10 pg/well (100 pg/mL). The results suggest that this ELISA is a reliable and quant. method to measure cellular MAGE-4 protein that is a potential target mol. for specific immunotherapy of human cancers.

IT Antigens

RL: ANT (Analyte); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(MAGE-4 (melanoma tumor-rejection antigen 4); establishment of ELISA for measuring cellular MAGE-4 protein on human cancers)

IT Neoplasm

(diagnosis; establishment of ELISA for measuring cellular MAGE-4 protein on human cancers)

IT Immunoglobulins

RL: ARG (Analytical reagent use); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(G, establishment of ELISA for measuring cellular MAGE-4 protein on human cancers)

IT Immunoassay

(enzyme-linked immunosorbent assay, establishment of ELISA for measuring cellular MAGE-4 protein on human cancers)

IT Antibodies

RL: ARG (Analytical reagent use); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(monoclonal, establishment of ELISA for measuring cellular MAGE-4 protein on human cancers)

L25 ANSWER 7 OF 10 CA COPYRIGHT 1997 ACS DUPLICATE 7

AN 123:336332 CA

TI Expression of the MAGE gene family in human lymphocytic leukemia

AU Shichijo, Shigeki; Tsunosue, Rika; Masuoka, Kazuhiro; Natori, Hideyo; Tamai, Makoto; Miyajima, Jiro; Sagawa, Kimitaka; Itoh, Kyogo

CS School Medicine, Kurume University, Fukuoka, 830, Japan

SO Cancer Immunol. Immunother. (1995), 41(2), 95-103

CODEN: CIIMDN; ISSN: 0340-7004

DT Journal

LA English

AB The MAGE gene family, encoding tumor-rejection antigens recognized by cytotoxic T lymphocytes, is frequently expressed in human solid cancers. However, its expression in leukemia has not been well studied. The authors have investigated MAGE gene expression at the mRNA level in human leukemia. The MAGE gene family was expressed in 17 of 34 (50%) examples of T cell leukemia (12/21 patients' peripheral blood mononuclear cells and 5/13 cell lines), in 7 of 16 (44%) cases of B cell leukemia (1/8 and 6/8

Searcher : Shears 308-4994

resp.), but in none of 23 myelomonocytic leukemia cases (0/16 and 0/7), as evaluated by the primers common to the **MAGE-1**, -3, -4 (-4a and/or -4b), and -6 genes and the semi-quant. reverse transcription/polymerase chain reaction method. None of a panel of normal lymphoid cells expressed the MAGE gene family. As revealed by the primers specific for each of the MAGE genes, the **MAGE-1**, -2, -3, -4 or -6 gene was expressed in 8, 8, 6, 2, or 6 resp. out of 23 types of leukemia cell lines.

Expression of the **MAGE-1 protein** in both the cell lines and patients' cells was confirmed by immunoblot anal. with the polyclonal antibody to recombinant **MAGE-1 protein**. Cellular **MAGE-4 protein** in the cell lines was measured by an ELISA with the polyclonal and **monoclonal** antibodies to recombinant **MAGE-4b protein**. In summary, the MAGE gene family was expressed in the substantial proportion of T cell leukemias, but in no case of myelomonocytic leukemia. **Antigens** coded by the MAGE gene family could be important mols. for understanding specific immunity against lymphocytic leukemia.

IT Gene, animal

RL: BPR (Biological process); BIOL (Biological study); PROC (Process)

(MAGE gene expression in human lymphocytic leukemia cells and cell lines)

IT Antigens

RL: BSU (Biological study, unclassified); BIOL (Biological study) (MAGE; gene expression in human lymphocytic leukemia cells and cell lines)

IT Leukemia

(B-cell, MAGE gene expression in human lymphocytic leukemia cells and cell lines)

IT Leukemia

(T-cell, MAGE gene expression in human lymphocytic leukemia cells and cell lines)

L25 ANSWER 8 OF 10 CA COPYRIGHT 1997 ACS

DUPLICATE 8

AN 120:131751 CA

TI Identification of the MAGE-1 gene product by **monoclonal** and polyclonal antibodies

AU Chen, Yao Tseng; Stockert, Elisabeth; Chen, Yachi; Garin-Chesa, Pilar; Rettig, Wolfgang J.; Van der Bruggen, P.; Boon, Thierry; Old, Lloyd J.

CS New York Unit, Ludwig Inst. Cancer Res., New York, NY, 10021, USA

SO Proc. Natl. Acad. Sci. U. S. A. (1994), 91(3), 1004-8

CODEN: PNASA6; ISSN: 0027-8424

DT Journal

LA English

AB The human MAG-1 gene encodes a melanoma **peptide**

antigen recognized by autologous cytotoxic T lymphocytes.

To produce antibodies against the **MAGE-1** gene

product, several approaches were taken. Three oligopeptides were synthesized based on predicted **MAGE-1** amino acid

sequences and were used to generate rabbit anti-**peptide**

anti-sera. In addn., a truncated **MAGE-1** cDNA

was cloned into an Escherichia coli expression vector, and

recombinant **protein** was produced and purified. All three

rabbit anti-**peptide** antisera showed reactivity against the

immunizing **peptide**, and one reacted with the recombinant

MAGE-1 protein by immunoblotting, but

none reacted with cell lysates from **MAGE-1**

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2/1/94
pc

mRNA-pos. cells. The recombinant **MAGE-1 protein** was then used for the generation of mouse **monoclonal** and rabbit polyclonal antibodies. One IgG1 **monoclonal** antibody, MA454, as well as rabbit polyclonal antisera recognized a 46-kDa **protein** in exts. of **MAGE-1** mRNA-pos. melanoma cell lines. The antibodies showed no apparent cross-reactivity with products of the closely related **MAGE-2** and **MAGE-3** genes. Serol. typing of normal and tumor cell lysates was in full agreement with mRNA anal., showing expression of **MAGE-1 protein** in **MAGE-1** mRNA-pos. testis and a subset of melanomas but not in **MAGE-1** mRNA-neg. normal or tumor tissues. Transfection of the **MAGE-1** gene into a **MAGE-1** mRNA-neg. melanoma cell line resulted in the expression of the 46-kDa **protein**, confirming the identity of this **protein** as the **MAGE-1** gene product.

IT **Proteins**, specific or class
RL: PREP (Preparation)
(gene **MAGE-1**, **monoclonal** and polyclonal antibodies to, prepn. and reactivity of)

IT Antibodies
RL: PREP (Preparation)
(to **MAGE-1** gene product, prepn. and reactivity of)

IT Antibodies
RL: PREP (Preparation)
(**monoclonal**, to **MAGE-1** gene product, prepn. and reactivity of)

L25 ANSWER 9 OF 10 CA COPYRIGHT 1997 ACS DUPLICATE 9

AN 122:262435 CA

TI **MAGE-1** gene product is a cytoplasmic **protein**

AU Schultz-Thater, Elke; Juretic, Antonio; Dellabona, Paolo; Luescher, Urs; Siegrist, Walter; Harder, Felix; Heberer, Michael; Zuber, Markus; Spagnoli, Giulio C.

CS Department of Surgery, University of Basel, Basel, Switz.

SO Int. J. Cancer (1994), 59(3), 435-9

CODEN: IJCNAW; ISSN: 0020-7136

DT Journal

LA English

AB **MAGE-1** gene encodes a human melanoma **antigen**, recognized by syngeneic cytotoxic T lymphocytes (CTL). **MAGE-1** transcripts are also detectable in breast cancers, in non-small cell lung carcinomas and in central nervous system tumors. To identify, in cellular preps., the **protein** encompassing the antigenic **peptide**, the authors generated a panel of **monoclonal** antibodies (**MAbs**) against the **MAGE-1** gene product by using, as immunogen, a full-length recombinant prepn. (rMAGE-1), obtained through expression cloning of the relevant gene in E. coli. Four reagents were obtained recognizing both rMAGE-1 and the 46-kDa native **protein** in cell lines expressing **MAGE-1** mRNA. No positivity could be detected in **MAGE-1**-mRNA-neg. melanoma lines. No surface labeling of **MAGE-1**-pos. cell lines could be obsd. In contrast, on permeabilization of MZ2 melanoma cells, all 4 **MAbs** induced efficient staining, as detected by cytofluorog. Fluorescence microscopy shows that **MAGE-1** gene product is a cytoplasmic **protein** clustered in paranuclear

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*published
01 Nov 1994
AL*

organelle-like structures. Thus, **MAGE-1**
protein location closely resembles that of P91A and P198
 murine-tumor **antigens**.

IT Gene, animal

RL: BSU (Biological study, unclassified); BIOL (Biological study)
 (**MAGE-1**; human **MAGE-1**
 gene **antigen** is cytoplasmic **protein** in
 melanoma)

IT **Antigens**

RL: ANT (Analyte); BOC (Biological occurrence); ANST (Analytical
 study); BIOL (Biological study); OCCU (Occurrence)
 (gene **MAGE-1**; human **MAGE-1**
 gene **antigen** is cytoplasmic **protein** in
 melanoma)

IT Cytoplasm

Melanoma

(human **MAGE-1** gene **antigen** is
 cytoplasmic **protein** in melanoma)

IT Antibodies

RL: BPN (Biosynthetic preparation); THU (Therapeutic use); BIOL
 (Biological study); PREP (Preparation); USES (Uses)
 (**monoclonal**, to gene **MAGE-1**
antigen; human **MAGE-1** gene
antigen is cytoplasmic **protein** in melanoma)

L25 ANSWER 10 OF 10 CA COPYRIGHT 1997 ACS DUPLICATE 10

AN 118:167452 CA

TI Cloning of genes for tumor rejection antigen precursors and their
 uses

IN Boon, Thierry; Van der Bruggen, Pierre; Van den Eynde, Benoit; Van
 Pel, Aline; De Plaen, Etienne; Lurquin, Christophe; Chomez, Patrick;
 Traversari, Catia

PA Ludwig Institute for Cancer Research, USA

SO PCT Int. Appl., 143 pp.

CODEN: PIXXD2

PI WO 9220356 A1 921126

DS W: AU, BB, BG, BR, CA, CS, FI, HU, JP, KP, KR, LK, MG, MW, NO, PL,
 RO, RU, SD, US

RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, DE, DK, ES, FR, GA, GB, GR,
 IT, LU, MC, ML, MR, NL, SE, SN, TD, TG

AI WO 92-US4354 920522

PRAI US 91-705702 910523

US 91-728838 910709

US 91-764364 910923

US 91-807043 911212

DT Patent

LA English

AB The genes or cDNA for tumor rejection antigen (TRA) precursors, e.g.
 the precursors for MAGE melanoma antigen, the P1A mastocytoma
 antigen, and the antigen F of human, and the murine counterpart of
 MAGE, smage, are cloned. The coding sequences of these TRA can be
 used for prepn. of vaccines by expression of the sequences alone or
 together with the gene for a cytokine, e.g., interleukin (IL)-2 or
 IL-4. They can also be expressed with a gene for an MHC or HLA
 antigen which presents the tumor rejection antigen derived from the
 precursor to the cytotoxic T cells. Expression of the TRA by tumor
 cells can lead to cell lysis mediated by the cytotoxic T cells that
 recognize the antigens. The TRA may be used for prepn. of
 pharmaceuticals, antibodies, and diagnostics for clin. applications.

IT Animal cell line

- IT (P1A.T2, mouse tumor rejection antigen P1A gene-contg.)
- IT Animal cell line
 - (P1A.TC3.1, mouse tumor rejection antigen P1A gene-contg.)
- IT Animal cell line
 - (PO.HTR, P815 tumor antigens A and B and C-deficient, transformation of, with mouse tumor rejection antigen)
- IT Melanoma
 - (antigens TRA of, of mouse or human, gene for, cloning of)
- IT Neoplasm
 - (diagnosis of, tumor rejection antigen precursors for)
- IT Mycobacterium BCG
 - (expression vector contg. DNA of, for antigen TRA gene)
- IT Virus
 - (expression vector derived from, for antigen TRA gene)
- IT Gene, animal
 - RL: PROC (Process)
 - (for antigens TRA, of human or mouse, cloning of)
- IT Mouse
 - (gene for antigens TRA of human or, cloning of)
- IT Lymphokines and Cytokines
 - RL: BIOL (Biological study)
 - (gene for, co-transformation of biol. pure cells with antigen TRA gene and)
- IT Polymerase chain reaction
 - (in detection of tumor rejection antigen precursor genes expression)
- IT Deoxyribonucleic acid sequences
 - Ribonucleic acid sequences
 - (of antigens TRA gene of human or mouse)
- IT Protein sequences
 - (of antigens TRA of mouse)
- IT Molecular cloning
 - (of gene for antigens TRA, of human or mouse)
- IT Immunity
 - (to cancers provoked by tumor rejection antigen precursors)
- IT Antibodies
 - RL: BIOL (Biological study)
 - (to tumor rejection antigen precursors)
- IT Bacteria
 - (transformation of, with antigen TRA gene)
- IT Animal tissue
 - Body fluid
 - (tumor rejection antigen precursor detection in, for monitoring cancerous state)
- IT Neoplasm inhibitors
 - Vaccines
 - (tumor rejection antigen precursors as)
- IT Histocompatibility antigens
 - RL: BIOL (Biological study)
 - (HLA, gene for, co-transformation of biol. pure cells with antigen TRA gene and)
- IT Histocompatibility antigens
 - RL: BIOL (Biological study)
 - (HLA-A1, gene for, co-transformation of biol. pure cells with tumor rejection antigen precursor gene and)
- IT Histocompatibility antigens
 - RL: BIOL (Biological study)
 - (MHC (major histocompatibility complex), gene for, transformation of biol. pure cells expressing, with antigen TRA gene)
- IT Lymphocyte

- (T-cell, cytotoxic, immune response of, to cancer cells, tumor rejection antigen precursors-provoked)
- IT Antigen
RL: BIOL (Biological study)
(TRA (tumor-rejection antigen), E, gene for, of human melanoma, cloning of)
- IT **Antigens**
RL: BIOL (Biological study)
(TRA (tumor-rejection antigen), **MAGE-1**, gene for, of human melanoma, cloning of)
- IT Antigen
RL: BIOL (Biological study)
(TRA (tumor-rejection antigen), MAGE-10, gene for, of human melanoma, cloning of)
- IT Antigen
RL: BIOL (Biological study)
(TRA (tumor-rejection antigen), MAGE-11, gene for, of human melanoma, cloning of)
- IT Antigen
RL: BIOL (Biological study)
(TRA (tumor-rejection antigen), MAGE-2, gene for, of human melanoma, cloning of)
- IT Antigen
RL: BIOL (Biological study)
(TRA (tumor-rejection antigen), MAGE-3, gene for, of human melanoma, cloning of)
- IT Antigen
RL: BIOL (Biological study)
(TRA (tumor-rejection antigen), MAGE-4, gene for, of human melanoma, cloning of)
- IT Antigen
RL: BIOL (Biological study)
(TRA (tumor-rejection antigen), MAGE-5, gene for, of human melanoma, cloning of)
- IT Antigen
RL: BIOL (Biological study)
(TRA (tumor-rejection antigen), MAGE-6, gene for, of human melanoma, cloning of)
- IT Antigen
RL: BIOL (Biological study)
(TRA (tumor-rejection antigen), MAGE-7, gene for, of human melanoma, cloning of)
- IT Antigen
RL: BIOL (Biological study)
(TRA (tumor-rejection antigen), MAGE-8, gene for, of human melanoma, cloning of)
- IT Antigen
RL: BIOL (Biological study)
(TRA (tumor-rejection antigen), MAGE-9, gene for, of human melanoma, cloning of)
- IT Antigen
RL: BIOL (Biological study)
(TRA (tumor-rejection antigen), PlA, gene for, of mouse mastocytoma, cloning of)
- IT Antigen
RL: BIOL (Biological study)
(TRA (tumor-rejection antigen), gene for, of human or mouse, cloning of)
- IT Antigen
RL: BIOL (Biological study)

- (TRA (tumor-rejection antigen), smage-I, gene for, of mouse melanoma, cloning of)
- IT Antigens
RL: BIOL (Biological study)
(TRA (tumor-rejection antigen), smage-II, gene for, of mouse melanoma, cloning of)
- IT Deoxyribonucleic acids
RL: BIOL (Biological study)
(complementary, of antigens TRA gene of human or mouse)
- IT Lymphokines and Cytokines
RL: BIOL (Biological study)
(interleukin 2, gene for, co-transformation of biol. pure cells with antigen TRA gene and)
- IT Lymphokines and Cytokines
RL: BIOL (Biological study)
(interleukin 4, gene for, co-transformation of biol. pure cells with antigen TRA gene and)
- IT Lymphokines and Cytokines
RL: BIOL (Biological study)
(interleukins, gene for, co-transformation of biol. pure cells with antigen TRA gene and)
- IT Antibodies
RL: BIOL (Biological study)
(**monoclonal**, to tumor rejection antigen precursors)
- IT Mast cell
(neoplasm, antigens TRA of, of mouse, gene for, cloning of)
- IT Genetic element
RL: BIOL (Biological study)
(promoter, antigen TRA gene expression in animal cells using)
- IT Virus, animal
(vaccinia, expression vector derived from, for antigen TRA gene)
- IT 136361-96-1, Antigen (mouse clone C1A.3.1 gene P1A reduced)
RL: BIOL (Biological study)
(amino acid sequence of and cloning of cDNA for, complete)
- IT 145882-36-6
RL: BIOL (Biological study)
(antigenic peptide for tumor rejection antigen P1A of A+B+ cells)
- IT 140101-03-7, Deoxyribonucleic acid (human clone B3 gene MAGE-1 plus 5'- and 3'-flanking region fragment) 146707-11-1 146707-12-2
146707-13-3 146707-15-5 146707-16-6 146707-18-8 146707-20-2
146707-22-4 146707-24-6 146707-25-7 146707-27-9 146707-29-1
146707-30-4 146707-32-6 146707-34-8 146707-36-0 146707-38-2
146707-40-6 146707-42-8
RL: BIOL (Biological study); PRP (Properties)
(nucleotide sequence and cloning of)
- IT 136362-51-1, Deoxyribonucleic acid (mouse clone C1A.3.1 gene P1A coding region) 146313-12-4, Deoxyribonucleic acid (human clone B3 gene MAGE-1) 146707-14-4 146707-17-7 146707-19-9 146707-21-3
146707-23-5 146707-26-8 146707-28-0 146707-31-5 146707-33-7
146707-35-9 146707-37-1 146707-39-3 146707-41-7
RL: BIOL (Biological study); PRP (Properties)
(nucleotide sequence and cloning of, complete)
- IT 146707-10-0
RL: PRP (Properties)
(nucleotide sequence of)

08/560024

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=> s mage(w) (1 or i) or mage1 or magei

L26	99	FILE BIOSIS
L27	93	FILE MEDLINE
L28	85	FILE EMBASE
L29	33	FILE LIFESCI
L30	12	FILE BIOTECHDS
L31	7	FILE WPIDS
L32	3	FILE CONFSCI
L33	0	FILE DISSABS
L34	96	FILE SCISEARCH
L35	21	FILE JICST-EPLUS
L36	124	FILE CANCERLIT

TOTAL FOR ALL FILES

L37 573 MAGE(W) (1 OR I) OR MAGE1 OR MAGEI

=> s l37(1) (polypeptide# or polyprotein# or protein# or peptide# or antigen#)

L38	83	FILE BIOSIS
L39	89	FILE MEDLINE
L40	82	FILE EMBASE
L41	32	FILE LIFESCI
L42	11	FILE BIOTECHDS
L43	7	FILE WPIDS
L44	2	FILE CONFSCI
L45	0	FILE DISSABS
L46	86	FILE SCISEARCH
L47	20	FILE JICST-EPLUS
L48	120	FILE CANCERLIT

TOTAL FOR ALL FILES

L49 532 L37(L) (POLYPEPTIDE# OR POLYPROTEIN# OR PROTEIN# OR PEPTIDE
Searcher : Shears 308-4994

08/560024

OR ANTIGEN#)

=> s 149 and (moab# or mab# or monoclon? or hybridom?)

L50 10 FILE BIOSIS
L51 10 FILE MEDLINE
L52 11 FILE EMBASE
L53 3 FILE LIFESCI
L54 2 FILE BIOTECHDS
L55 2 FILE WPIDS
L56 0 FILE CONFSCI
L57 0 FILE DISSABS
L58 15 FILE SCISEARCH
L59 1 FILE JICST-EPLUS
L60 12 FILE CANCERLIT

TOTAL FOR ALL FILES

L61 66 L49 AND (MOAB# OR MAB# OR MONOCLON? OR HYBRIDOM?)

=> dup rem l61

PROCESSING COMPLETED FOR L61

L62 27 DUP REM L61 (39 DUPLICATES REMOVED)

=> d 1-27 bib abs; fil uspat; s l61

L62 ANSWER 1 OF 27 SCISEARCH COPYRIGHT 1997 ISI (R)
AN 96:448460 SCISEARCH
GA The Genuine Article (R) Number: UQ455
TI SEROLOGICAL ANALYSIS OF MELAN-A(MART-1), A MELANOCYTE-SPECIFIC
PROTEIN HOMOGENEOUSLY EXPRESSED IN HUMAN MELANOMAS
AU CHEN Y T (Reprint); STOCKERT E; JUNGBLUTH A; TSANG S L; COPLAN K A;
SCANLAN M J; OLD L J
CS MEM SLOAN KETTERING CANC CTR, NEW YORK BRANCH, LUDWIG INST CANC RES,
1275 YORK AVE, NEW YORK, NY, 10021 (Reprint); NEW YORK HOSP, CORNELL
MED CTR, DEPT PATHOL, NEW YORK, NY, 10021
CYA USA
SO PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES
OF AMERICA, (11 JUN 1996) Vol. 93, No. 12, pp. 5915-5919.
ISSN: 0027-8424.
DT Article; Journal
FS LIFE
LA ENGLISH
REC Reference Count: 29
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS
AB Recent progress in the structural identification of human
melanoma antigens recognized by autologous cytotoxic T cells has led
to the recognition of a new melanocyte differentiation antigen,
Melan-A(MART-1). To determine the properties of the Melan-A gene
product, Melan-A recombinant protein was produced in Escherichia
coli and used to generate mouse **monoclonal** antibodies (
mAbs). Two prototype mAbs, A103 and A355, were selected for
detailed study. Immunoblotting results with A103 showed a 20-22-kDa
doublet in Melan-A mRNA positive melanoma cell lines and no
reactivity with Melan-A mRNA-negative cell lines. A355, in addition
to the 20-22-kDa doublet, recognized several other protein species
in Melan-A mRNA-positive cell lines. Immunocytochemical assays on
cultured melanoma cells showed specific and uniform cytoplasmic
staining in Melan-A mRNA-positive cell lines, Immunohistochemical
analysis of normal human tissues with both **mAbs** showed
staining of adult melanocytes and no reactivity with the other
normal tissues tested, Analysis of 21 melanoma specimens showed
Searcher : Shears 308-4994

homogenous staining of tumor cell cytoplasm in 16 of 17 Melan-A mRNA-positive cases and no reactivity with the three Melan-A mRNA-negative cases.

L62 ANSWER 2 OF 27 CANCERLIT

AN 96633172 CANCERLIT

TI **Monoclonal** antibodies against full-length **MAGE-1 protein** identify a crossreacting 72 kD **antigen** which is coexpressed with **MAGE-1** in melanoma cells (Meeting abstract).

AU Carrel S; Salvi S; Hartmann F; Rimoldi D; Schreyer M; Spagnoli G
CS Ludwig Inst. for Cancer Res., Lausanne Branch, Univ. of Lausanne, 1066 Epalinges, Switzerland.

SO Proc Annu Meet Am Assoc Cancer Res, (1996). Vol. 37, pp. A3172.
ISSN: 0197-016X.

DT (MEETING ABSTRACT)

FS ICDB

LA English

EM 9608

AB To study the expression of the **MAGE-1 protein** in various melanoma tumors, we produced **monoclonal** antibodies (**Mabs**) against a full-length recombinant **MAGE-1** product. The **hybridoma** supernatants were screened for a selective reactivity by immunocytochemistry on **MAGE-1+** cell lines. **Mabs** from 2 **hybridomas** were found to stain only **MAGE-1+** and not **MAGE-1-** cells. Further testing of these 2 **Mabs** by Western blotting showed that they selectively stained two major **protein** bands of approximately 46 and 72 kD in the lysates of 10 different **MAGE-1+** melanoma cells. The 46 kD **protein** is likely to be the **MAGE-1 protein**, since it corresponds to its expected MW and it was the **protein** detected in lysates of **MAGE-1** negative cell lines after they were transfected with **MAGE-1** cDNA. The 72 kD **protein** does not appear to be encoded by **MAGE-1-4** since it was not detectable either in the above **MAGE-1** transfectant or in **MAGE-1** negative melanoma cells transiently transfected with **MAGE-2**, 3, 4 or 12 cDNA. The fact that the 72 kD is selectively stained by the two **Mabs** each directed against the recombinant **MAGE-1 protein** indicate that the 72 kD **protein** must share common antigenic determinant(s) with **MAGE-1 protein**, suggesting that the 72 kD **MAGE-1** crossreacting **antigen** (**MAGE-1/72 CA**) belong to the **MAGE** family. Furthermore the fact that **MAGE-1/72 CA** is coexpressed in 11 **MAGE-1+** cell lines strongly suggests that the expression of the two **proteins** are under the same regulatory control. Recently the presence of **MAGE-1** and of the 72 kD **protein** could be identified by Western blotting in lysates of normal testis.

L62 ANSWER 3 OF 27 BIOSIS COPYRIGHT 1997 BIOSIS

AN 96:257272 BIOSIS

DN 98813401

TI **Monoclonal** antibodies against full-length **MAGE-1 protein** identify a crossreacting 72 kDa **antigen** which is coexpressed with **MAGE-1**

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melanoma cells.

AU Carrel S; Salvi S; Hartmann F; Rimoldi D; Schreyer M; Spagnoli G
 CS Ludwig Inst. Cancer Res., Lausanne Branch, Univ. Lausanne, 1066
 Epalinges, Switzerland
 SO 87th Annual Meeting of the American Association for Cancer Research,
 Washington, D.C., USA, April 20-24, 1996. Proceedings of the American
 Association for Cancer Research Annual Meeting 37 (0). 1996. 465.
 ISSN: 0197-016X
 DT Conference
 LA English

L62 ANSWER 4 OF 27 BIOSIS COPYRIGHT 1997 BIOSIS DUPLICATE 1

AN 96:415356 BIOSIS

DN 99137712

TI **Monoclonal** antibodies against recombinant-**MAGE-1** protein identify a cross-reacting 72-kDa antigen which is co-expressed with **MAGE-1** protein in melanoma cells.

AU Carrel S; Schreyer M; Spagnoli G; Cerottini J-C; Rimoldi D
 CS Ludwig Inst. Cancer Res., Ch. des Boveresses 155, 1066 Epalinges,
 Switzerland

SO International Journal of Cancer 67 (3). 1996. 417-422. ISSN:
 0020-7136

LA English

AB The **MAGE-I** gene codes for tumor-associated peptides recognized by cytolytic T lymphocytes in association with MHC-class-I molecules such as HLA-A I and HLA-Cw16. In the course of a study aiming at the immunohistochemical detection of the **MAGE-I** gene product in tumor samples, 2 mouse monoclonal antibodies (**MABs**) directed against a full-length recombinant **MAGE-I** fusion protein were found to react strongly not only with the 46-kDa **MAGE-I** protein, but also with a 72-kDa product in immunoblots of lysates obtained from several **MAGE1**-mRNA-positive melanoma cell lines. Pre-incubation of the antibodies with the recombinant **MAGE-I** fusion protein abolished their reactivity both with **MAGE-I** protein and with the 72-kDa product, thus confirming the occurrence of antigenic determinant(s) shared by the 2 proteins. The 72-kDa protein is not an alternative product of **MAGE-I**, since it was still detected in lysates of a **MAGE-I** loss variant derived from a **MAGE-I**-positive melanoma cell line. Moreover, the 72-kDa protein does not appear to be a product of the other members of the MAGE gene family known to be expressed in tumors (such as MAGE-2, -3, -4 and -12). Interestingly, expression of the 72-kDa protein was found to be correlated with that of **MAGE-I** protein. Thus, in 30 tumor cell lines analyzed by immunoblotting and RT-PCR, the 72-kDa protein was never detected in **MAGE-I**-mRNA-negative cell lines, while it was co-expressed with **MAGE-I** protein in 12 out of 15 cell lines expressing **MAGE-I**. Furthermore, the 72-kDa protein was detected in lysates of human testis, the only normal tissue known to express **MAGE-I**. Finally, treatment of **MAGE-1**-mRNA-negative cell lines with 5-Aza-2'-deoxycytidine, a hypomethylating agent known to induce **MAGE-I** expression, resulted in the expression of the 72-kDa protein. Taken collectively, these findings suggest that expression of the gene encoding the 72-kDa protein identified in this study

Searcher : Shears 308-4994

through antigenic determinant(s) shared with **MAGE-I** protein is regulated in a way similar to that of **MAGE-I**.

L62 ANSWER 5 OF 27 SCISEARCH COPYRIGHT 1997 ISI (R)
 AN 96:537640 SCISEARCH
 GA The Genuine Article (R) Number: UX080
 TI METASTATIC POTENTIAL OF HUMAN-MELANOMA CELLS IN NUDE-MICE -
 CHARACTERIZATION OF PHENOTYPE, CYTOKINE SECRETION AND
 TUMOR-ASSOCIATED ANTIGENS
 AU SCHADENDORF D (Reprint); FICHTNER I; MAKKI A; ALIJAGIC S; KUPPER M;
 MROWIETZ U; HENZ B M
 CS HUMBOLDT UNIV BERLIN, VIRCHOW CLIN, DEPT DERMATOL, AUGUSTENBURGER PL
 1, D-13344 BERLIN, GERMANY (Reprint); MAX DELBRUCK CTR MOLEC MED,
 D-13125 BERLIN, GERMANY; UNIV CLIN KIEL, DEPT DERMATOL, D-24105
 KIEL, GERMANY
 CYA GERMANY
 SO BRITISH JOURNAL OF CANCER, (JUL 1996) Vol. 74, No. 2, pp. 194-199.
 ISSN: 0007-0920.
 DT Article; Journal
 FS LIFE; CLIN
 LA ENGLISH
 REC Reference Count: 44

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Incidence and mortality of human malignant melanoma has risen rapidly over recent decades. Although the notorious resistance to treatment is characteristic for metastatic malignant melanoma, only a few experimental models have been established to study the metastatic cascade or to test new alternative treatment modalities. Thus, new human models are wanted. Here, we describe the metastatic behaviour of seven human melanoma cell lines derived from two primary cutaneous melanomas (WM 98-1, WM 1341) and five metastases established from liver (UKRV-Mel-4), skin (M7, M13), pleural effusion (UKRV-Mel-2) and lymph node (MV3). All cell lines were analysed for their capacity to grow in nude mice after s.c. and i.v. administration. M13 cells developed liver metastases spontaneously after s.c. injection, and subsequent passages of M13 and M7 melanoma cells caused liver metastases after i.v. injection, whereas MV3 and WM 98-1 gave rise to lung metastases, using the same inoculation route. In contrast, WM 1341, UKRV-Mel-2 and UKRV-Mel-4 grew only very slowly in nude mice after s.c. injection and did not cause any metastases after i.v. or s.c. administration. The pattern of metastases or growth kinetics did not correlate with the interleukin 8 or tumour necrosis factor secretion of cell lines. Adhesion molecules and growth factor receptor expression on the cell lines differed widely, as determined by flow cytometry, with the low metastatic cell lines (UKRV-Mel-2, UKRV-Mel-4 and WM 1341) demonstrating a marked reduction in VLA-1 and VLA-5 expression compared with the metastatic lines (M7, M13, MV3 and WM 98-1). Expression of pigment-related **proteins** such as tyrosinase, TRP-1, TRP-2, Melan-A/MART-1, gp100, **MAGE1** or **MAGE-3** was not associated with growth and metastatic characteristics of the melanoma cell lines analysed. In conclusion, the established human melanoma cell lines exhibited diverse growth behaviour in nude mice in congruence with some early established prognostic markers such as VLA-1 and VLA-5. The xenografts provide good models for further study of metastatic processes as well as for evaluative alternative treatment modalities including new pharmaceutical drugs and gene therapeutic targeting using tissue-specific gene regulatory elements for gene targeting.

L62 ANSWER 6 OF 27 BIOSIS COPYRIGHT 1997 BIOSIS DUPLICATE 2
 AN 96:563309 BIOSIS
 DN 99292665
 TI The tumour-associated **antigen MAGE-1** is detectable in formalin-fixed paraffin sections of malignant melanoma.
 AU Gudat F; Zuber M; Durmuller U; Kocher T; Schaefer C; Noppen C; Spagnoli G
 CS Inst. Pathol., Univ. Basel, Schonbeinstrasse 40, CH-4003 Basel, Switzerland
 SO Virchows Archiv 429 (2-3). 1996. 77-81. ISSN: 0945-6317
 LA English
 AB The **MAGE-1** gene encodes a **protein** encompassing a HLA-A1-restricted target epitope for cytolytic T lymphocytes. **Monoclonal** antibodies directed against the **MAGE-1 protein** were tested for usage in immunohistology of routine pathology material. Seven formalin-fixed, paraffin-embedded malignant melanomas were studied by the Avidin-Biotin complex (ABC) method with or without different **antigen** retrieval methods. Native, frozen tissues from the same tumours were used to validate the results by immunohistochemistry on frozen sections, by PCR for mRNA and by **protein** demonstration in tissue extracts using western blotting. Of 4 **monoclonal** antibodies tested, **mAB** 34B and **mAB** 77B were highly efficient in detecting **MAGE-1 protein** in deparaffinized sections with the regular ABC method after microwave pretreatment. In a series of an additional 28 patients 75% expressed **MAGE-1**, 50% in a substantial proportion. Follow-up studies in 6 patients indicate that the expression pattern remains stable but may change substantially within a short range. Immunohistology is thus a rapid and well-established method that might be used to select and monitor HLA-A1 positive patients with malignant melanoma and other candidate tumours for **MAGE-1**-directed immuno-therapy.

L62 ANSWER 7 OF 27 BIOTECHDS COPYRIGHT 1997 DERWENT INFORMATION LTD
 AN 95-12604 BIOTECHDS
 TI New **monoclonal** antibody binding to tumor rejection **antigen** precursor **MAGE-1**; production from **hybridoma** for use as a diagnostic agent, and recombinant **MAGE-1** for use as an immunogen
 AU Chen Y T; Stockert E; Chen Y; Garin-Chesa P; Rettig W J; van der Bruggen P; Boon-Falleur T; Old L J
 PA Ludwig-Inst.Cancer-Res.; Mem.Sloan-Kettering-Cancer-Cent.
 PI WO 9520974 10 Aug 1995
 AI WO 95-US95 5 Jan 1995
 PRAI US 94-190411 1 Feb 1994
 DT Patent
 LA English
 OS WPI: 95-283606 [37]
 AN 95-12604 BIOTECHDS
 AB A new **monoclonal** antibody (**Mab**), MA454, binds specifically to tumor rejection **antigen** precursor **MAGE-1**, and is produced by a **hybridoma** cell culture. The **Mab** may be used to determine **MAGE-1** in a sample, by binding to a solid phase, labeling and detecting binding. An isolated **MAGE-1** tumor rejection **antigen** precursor, which is a glycoprotein of mol.wt. 46,000 (SDS-PAGE) or may be in recombinant
 Searcher : Shears 308-4994

form (mol.wt. 34,300) is also new, and has a specified **protein** sequence, encoded by a specified DNA sequence. The **antigen** may be used in an immunogenic composition with an adjuvant. (29pp)

- L62 ANSWER 8 OF 27 EMBASE COPYRIGHT 1997 ELSEVIER SCI. B.V.
 AN 95248406 EMBASE
 TI Identification of **MAGE-1** and **MAGE-4**
proteins in spermatogonia and primary spermatocytes of
 testis.
 AU Takahashi K.; Shichijo S.; Noguchi M.; Hirohata M.; Itoh K.
 CS Department of Immunology, Kurume University School of Medicine, 67
 Asahi-machi, Kurume 830, Japan
 SO Cancer Research, (1995) 55/16 (3478-3482).
 ISSN: 0008-5472 CODEN: CNREA8
 CY United States
 DT Journal
 FS 016 Cancer
 026 Immunology, Serology and Transplantation
 028 Urology and Nephrology
 029 Clinical Biochemistry
 LA English
 SL English
 AB The **MAGE** genes encoding tumor rejection **antigens**
 recognized by CTLs are expressed at the mRNA level in various
 cancers and in the testis but not in the other normal tissues. The
 expression of **MAGE-1** or **MAGE-4 protein**
 in the testicular cells was studied immunohistochemically with the
 antibodies to the recombinant **MAGE-1** or **MAGE-4**
protein. Both **proteins** were identified in the
 nucleus and cytoplasm of spermatogonia and in primary spermatocytes
 but not in spermatids or Sertoli's cells. Therefore, **MAGE**
proteins are normal tissue **antigens**
 compartmentalized in particular testicular cells playing an
 important role in the early phase of the spermatogenesis.
- L62 ANSWER 9 OF 27 CANCERLIT
 AN 96610627 CANCERLIT
 TI Immunohistochemical localization of **MAGE-1** in melanoma cell lines by
monoclonal anti-**MAGE-1** antibodies (Meeting abstract).
 AU Carrel S; Hartmann F; Salvi S; Spagnoli G; Schreyer M; Rimoldi D
 CS Ludwig Inst. for Cancer Research, Lausanne Branch, Univ. of
 Lausanne, 1066 Epalinges, Switzerland.
 SO Proc Annu Meet Am Assoc Cancer Res, (1995). Vol. 36, pp. A2854.
 ISSN: 0197-016X.
 DT (MEETING ABSTRACT)
 FS ICDB
 LA English
 EM 9604
 AB The human **MAGE-1** gene codes for a melanoma
peptide antigen recognized by cytotoxic
 T-lymphocytes. In order to assess the expression of the **MAGE**
-1 protein in melanoma tumors, we produced
monoclonal antibodies against the **MAGE-1**
 gene product by immunizing mice with a full length recombinant
MAGE-1 protein. The **hybridoma**
 products were screened for reactivity with the recombinant
MAGE-1 protein by ELISA and by
 immunohistochemistry on a panel of **MAGE-1** mRNA
 positive and negative cell lines. Seven antibodies were chosen on
 Searcher : Shears 308-4994

the basis of their selective reactivity for **MAGE-1** mRNA positive cell lines. By immunoblotting the selected antibodies reacted with the recombinant **MAGE-1 protein** used for immunization and with nonidet P40 cell lysates from **MAGE-1** mRNA positive cell lines but not with lysates from **MAGE-1** negative cells. All **monoclonal** antibodies recognized a **protein** of approximately 46 kD in the extracts of **MAGE-1** mRNA-positive melanoma cell lines. In addition, the **monoclonal** antibodies reacted positively with a **MAGE-1** negative melanoma line or P815 mouse mastocytoma cells transfected with the **MAGE-1** gene. These antibodies are being tested on tissue sections from **MAGE-1** mRNA positive and negative tumors.

L62 ANSWER 10 OF 27 BIOSIS COPYRIGHT 1997 BIOSIS DUPLICATE 4

AN 95:317017 BIOSIS

DN 98331317

TI Identification and intracellular location of MAGE-3 gene product.

AU Kocher T; Schultz-Thater E; Gudat F; Schaefer C; Casorati G; Juretic A; Willimann T; Harder F; Heberer M; Spagnoli G C

CS Surg. Res. Lab., 20 Hebelstrasse 4031 Basel, Switzerland

SO Cancer Research 55 (11). 1995. 2236-2239. ISSN: 0008-5472

LA English

AB The human MAGE-3 gene encodes a melanoma antigenic epitope recognized by specific cytotoxic T lymphocytes, but its gene product has not been identified thus far. We produced a recombinant MAGE-3 gene product by expression cloning of the entire reading frame in the context of a fusion **protein** characterized by a 10-histidine tail, allowing purification by metal chelation on a nickel Sepharose column. The semipurified product was used to generate MAGE-3-specific **monoclonal** antibodies. One reagent could identify by immunoblotting the native MAGE-3 gene product as a M, 48,000 **protein** in lysates of cell lines showing evidence of MAGE-3 gene expression. No apparent cross-reactivity with recombinant or native **MAGE-1** gene product was observed. Immunohistochemistry shows that, closely resembling the **MAGE-1** gene product, MAGE-3 is a cytoplasmic **protein**.

L62 ANSWER 11 OF 27 BIOSIS COPYRIGHT 1997 BIOSIS

AN 96:46201 BIOSIS

DN 98618336

TI A 72kDa **protein** coexpressed in melanoma cells with

MAGE-1, revealed by anti-recombinant **MAGE**

-1 monoclonal antibodies.

AU Carrel S; Hartmann F; Salvi S; Spagnoli G; Schreyer M; Rimoldi D

CS Ludwig Inst. Cancer Research, Lausanne Branch, Univ. Lausanne, 1066 Epalinges, Switzerland

SO Fifth International Conference of Anticancer Research, Corfu, Greece, October 17-22, 1995. Anticancer Research 15 (5A). 1995. 1672. ISSN: 0250-7005

DT Conference

LA English

L62 ANSWER 12 OF 27 CANCERLIT

AN 96624964 CANCERLIT

TI A 72 kD **protein** coexpressed in melanoma cells with

MAGE-1, revealed by anti-recombinant **MAGE**

-1 monoclonal antibodies (Meeting abstract).

AU Carrel S; Hartmann F; Salvi S; Spagnoli G; Schreyer M; Rimoldi D

Searcher : Shears 308-4994

08/560024

CS Ludwig Inst. for Cancer Res., Lausanne Branch, Univ. of Lausanne,
1066 Epalinges, Switzerland.

SO Anticancer Res, (1995). Vol. 15, No. 5A, pp. 1672.
ISSN: 0250-7005.

DT (MEETING ABSTRACT)

FS ICDB

LA English

EM 9608

AB The human **MAGE-1** gene codes for a melanoma
peptide antigen recognized by cytotoxic
T-lymphocytes. In order to assess the expression of the **MAGE**
-1 protein in melanoma tumors, we produced
monoclonal antibodies against a full-length recombinant
MAGE-1 gene product. The **hybridoma**
products were screened for a selective reactivity by
immunohistochemistry on **MAGE-1+** and **MAGE**
-1- cell lines. Antibodies from 3 hybrids were found to
stain only **MAGE-1+** cell. Further
characterization of these antibodies by Western blotting using NP40
lysates from cell lines showed that two of them (6C1 and 6F12)
reacted with two major **proteins** of approx 46 and 72 kD in
lysates of **MAGE-1+** melanoma cells. The 46 kD
protein corresponded to the product of the **MAGE-**
1 gene, since an identical **protein** appeared in
MAGE-1 negative cell lines following transiently
transfected with **MAGE-2**, 3, 4 or 12 cDNA. The presence of a 72 kD
protein coexpressed with **MAGE-1** in
melanoma cells represents a new finding. The question whether this
protein represents another member of the MAGE family remains
open. Whatever the final outcome is the 72 kD **protein** by
definition has to share a common epitope with **MAGE-**
1. The coexpression of **MAGE-1** and of the
72 kD **protein** was further observed in 10 out of 11
MAGE-1+ melanoma lines. In 10 **MAGE-**
1- melanoma lines either the 46 kD nor the 72 kD
protein was detected by **mab** 6C1 and 6F12. More
recently the presence of the 72 kD **protein** and of
MAGE-1 could be identified by Western blotting in
normal testis.

L62 ANSWER 13 OF 27 SCISEARCH COPYRIGHT 1997 ISI (R)

AN 95:51965 SCISEARCH

GA The Genuine Article (R) Number: QA636

TI MELANOMA PATIENTS IMMUNIZED WITH MELANOMA CELL VACCINE INDUCE
ANTIBODY-RESPONSES TO RECOMBINANT **MAGE-1**
ANTIGEN

AU HOON D S B (Reprint); YUZUKI D; HAYASHIDA M; MORTON D L

CS JOHN WAYNE CANC INST, DIV MOLEC & CELLULAR IMMUNOL, 2200 SANTA
MONICA BLVD, SANTA MONICA, CA, 90404 (Reprint); ST JOHNS HOSP, JOHN
WAYNE INST CANC TREATMENT & RES, SANTA MONICA, CA, 90404

CYA USA

SO JOURNAL OF IMMUNOLOGY, (15 JAN 1995) Vol. 154, No. 2, pp. 730-737.
ISSN: 0022-1767.

DT Article; Journal

FS LIFE

LA ENGLISH

REC Reference Count: 34
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB The **MAGE-1** gene was recently characterized to
encode an immunogenic tumor Ag on several types of human tumors,
Searcher : Shears 308-4994

including melanoma. This Ag is expressed in a wide variety of human tumors and not in normal cells, except testicular tissue, as assessed through specific mRNA analysis. In this study we cloned the **MAGE-1** gene exon 3 region from a colon carcinoma cell line and expressed it in *Escherichia coli*. The recombinant **MAGE-1 protein** was affinity purified. By using Western blot analysis, IgG and IgM anti-**MAGE-1** Abs were detected in the sera of melanoma patients. Fifty-three patients immunized with a melanoma cell vaccine (MCV) were assessed for anti-**MAGE-1** IgG responses by using a **MAGE-1** Ag-specific ELISA. The MCV consisted of three melanoma cell lines that expressed **MAGE-1**. Comparisons of anti-**MAGE-1** IgG response pre-MCV treatment with 12- to 16-wk post-MCV treatment were made. Fifty-seven percent of the patients immunized with the MCV showed significant enhancement of IgG response to recombinant **MAGE-1 protein**. Patients who responded had no particular HLA-A or -B allele expression pattern. Melanoma patients immunized with whole cell MCV containing **MAGE-1** can enhance anti-**MAGE-1** IgG Abs. Recombinant **MAGE-1 protein** can be used to assess patient response to **MAGE-1** and will be investigated as a potential cancer vaccine against a wide variety of human tumors that express **MAGE-1**.

L62 ANSWER 14 OF 27 SCISEARCH COPYRIGHT 1997 ISI (R)
 AN 95:138920 SCISEARCH
 GA The Genuine Article (R) Number: QF831
 TI SERUM IMMUNOGLOBULINS SPECIFIC FOR INTRACELLULAR PROTEINS OF
 SQUAMOUS-CELL CARCINOMA
 AU CALENOFF E (Reprint); CHEEVER M A; SATAM M; DUTRA J C; PELZER H J;
 KERN R C; HANSON D G
 CS NORTHWESTERN UNIV, SCH MED, DEPT OTOLARYNGOL HEAD & NECK SURG, BASIC
 & APPL IMMUNOL LAB, CHICAGO, IL, 60611 (Reprint); UNIV WASHINGTON,
 DEPT MED, DIV ONCOL, SEATTLE, WA, 98195
 CYA USA
 SO ARCHIVES OF OTOLARYNGOLOGY-HEAD & NECK SURGERY, (FEB 1995) Vol. 121,
 No. 2, pp. 183-191.
 ISSN: 0886-4470.
 DT Article; Journal
 FS LIFE; CLIN
 LA ENGLISH
 REC Reference Count: 43
 ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS
 AB Objective: To determine an autologous humoral immune response to
 squamous cell carcinoma (SCC) intracellular proteins in patients
 with SCC.
 Design: Intracellular proteins were isolated from 25 different
 cultured SCC lines. The proteins were used as a source of antigens
 to measure IgA, IgE, and IgG responses in the serum samples of
 patients and controls. Antibody response was assessed in both
 unfractionated and fractionated intracellular proteins.
 Patients: The serum samples of 65 patients with SCC and of 65
 age- and gender-matched controls were tested.
 Results: Antibodies to SCC intracellular proteins were detected
 in the serum samples of 40 (62%) of the 65 patients with SCC and in
 the serum samples of 46 (71%) of 65 controls. Thirty (46%) of the
 patients with SCC and 40 (62%) of the controls had IgE responses, 18
 (28%) of the patients and one (2%) of the controls had IgA
 responses, and 17 (26%) of the patients and 14 (22%) of the controls
 Searcher : Shears 308-4994

had IgG responses. An inverse relation was noted between detectable IgE responses and IgA or IgG responses in the patients and the controls. The analysis of antibody response indicated that 28 molecules were recognized predominantly by the serum samples of patients with SCC, but not by the serum samples of controls.

Conclusions: A substantial proportion of patients with SCC and of controls exhibited an autologous humoral immune response to SCC intracellular proteins. The IgE responses to SCC intracellular proteins were inversely related to IgA or to IgG responses. Different antibody isotypes normally cause markedly different immune functions, and may suggest different roles for the existent immune responses to SCC antigens. We identified many tumor-associated antigens that were selectively recognized by the serum samples of patients with SCC. These antigens could be used to define molecular studies of immune surveillance and selection, and may represent appropriate targets for immunotherapy.

L62 ANSWER 15 OF 27 BIOSIS COPYRIGHT 1997 BIOSIS DUPLICATE 5
 AN 95:411919 BIOSIS
 DN 98426219
 TI Detection of MAGE-4 protein in lung cancers.
 AU Shichijo S; Hayashi A; Takamori S; Tsunosue R; Hoshino T; Sakata M; Kuramoto T; Oizumi K; Itoh K
 CS Dep. Immunol., Kurume Univ. Sch. Med., 67 Asahi-machi, Kurume 830, Japan
 SO International Journal of Cancer 64 (3). 1995. 158-165. ISSN: 0020-7136
 LA English
 AB Expression of genes of the MAGE family, which encode tumor-rejection **antigens** recognized on HLA-A1 and -Cw1601 by cytotoxic T lymphocytes (CTL), was investigated in lung cancers at the mRNA (**MAGE-1, -2, -3/-6, and -4 (4a and/or 4b)) and protein (MAGE-4) levels. MAGE-1, -2, -3/-6 and -4 genes were expressed, respectively, at the mRNA level in 6, 7, 20 and 7 of 53 lung cancers (SO non-small-cell lung cancers and 3 small-cell lung cancers) by the reverse transcription-polymerase chain reaction (RT-PCR) method. Polyclonal antibody (Ab) and monoclonal antibody (MAb) against recombinant MAGE-4b protein were developed to detect MAGE-4 protein. Both the polyclonal Ab and the RS MAb recognized a 45-kDa protein in extracts of MAGE-4 mRNA-positive lung cancers, and showed no apparent cross-reactivity with the other MAGE gene products except with MAGE-4a by immunoblot analyses and transfection experiments. MAGE-4 protein was detected on 13 of 44 (30%) lung cancers (18 to 55,989 pg/mg) by ELISA with the polyclonal Ab and RS MAb. These 13 lung cancers consisted of 6 of 6 MAGE-4 mRNA-detectable and 7 of 38 MAGE-4 mRNA undetectable lung cancers. Histologically, these comprised 7 of 10 squamous-cell carcinomas, 4 of 30 adenocarcinomas and 2 of 3 small-cell lung cancers. The proportions of MAGE gene-positive samples, at both the mRNA and protein levels, correlated with the size of the primary tumors and with regional node involvement. These results should provide important information on specific immunotherapy of lung cancers using MAGE gene products.**

L62 ANSWER 16 OF 27 BIOSIS COPYRIGHT 1997 BIOSIS DUPLICATE 6
 AN 95:551277 BIOSIS
 DN 98565577
 TI Establishment of an enzyme-linked immunosorbent assay (ELISA) for measuring cellular MAGE-4 protein on human cancers.
 Searcher : Shears 308-4994

AU Shichijo S; Tsunosue R; Kubo K; Kuramoto T; Tanaka Y; Hayashi A; Itoh K
 CS Dep. Immunol., Kurume Univ. Sch. Med., Kurume 830, Japan
 SO Journal of Immunological Methods 186 (1). 1995. 137-149. ISSN: 0022-1759
 LA English
 AB The MAGE genes encoding tumor-rejection **antigens** are expressed on various human cancers. An enzyme-linked immunosorbent assay (ELISA) was established for measuring cellular MAGE-4 **protein** (MAGE-4a and/or -4b) expressed on human tumor cells using a **monoclonal** antibody (**mAb**) and polyclonal Ab to recombinant MAGE-4b **protein**. Both the R5 **mAb** (IgG1) and the polyclonal Ab recognized a 45 kDa **protein** in extracts of MAGE-4 mRNA positive cancers, and showed no apparent cross-reactivity to the other MAGE gene products (**MAGE-1, -2, -3, -6, and -12**) by the immunoblot analyses. The R5 **mAb** and the polyclonal Ab primarily recognized one (the position 119-133) and two oligopeptides (the positions 119-133 and 259-273), respectively, among a series of 31 different MAGE-4b oligopeptides. The amino acid sequences of these two **peptides** were identical to those of MAGE-4a and -4b, but differed from those of all the other MAGE **proteins** (**MAGE-1, -2, -3, -6, and -12**). Substitution of glycine for amino acid in position 123 (arginine, R), 124 (lysine, K), 126 (R) or 128 (K) in a MAGE-4b oligopeptide of the position 119-132 severely decreased the reactivity of the R5 **mAb** to the oligopeptide. This ELISA also showed no apparent cross-reactivity with the other MAGE gene products (**MAGE-1, -2 -3, -6, and -12**). The minimum detectable level of MAGE-4 **protein** was determined to be 10 pg/well (100 pg/ml). The results suggest that this ELISA is a reliable and quantitative method to measure cellular MAGE-4 **protein** that is a potential target molecule for specific immunotherapy of human cancers.

L62 ANSWER 17 OF 27 SCISEARCH COPYRIGHT 1997 ISI (R)
 AN 95:527668 SCISEARCH
 GA The Genuine Article (R) Number: RM035
 TI BIOLOGIC, IMMUNOCYTOCHEMICAL, AND CYTOGENETIC CHARACTERIZATION OF 2 NEW HUMAN-MELANOMA CELL-LINES - IIB-MEL-LES AND IIB-MEL-IAN
 AU KAIRIYAMA C; SLAVUTSKY I; LARRIPA I; MORVILLO V; BRAVO A I; BOVER L; PODHAJECER O L; MORDOH J (Reprint)
 CS FDN CAMPOMAR, INST INVEST BIOQUIM, AV PATRICIAS ARGENTINAS 435, RA-1405 BUENOS AIRES, DF, ARGENTINA (Reprint); FDN CAMPOMAR, INST INVEST BIOQUIM, RA-1405 BUENOS AIRES, DF, ARGENTINA; UNIV BUENOS AIRES, FAC CIENCIAS EXACTAS & NAT, RA-1405 BUENOS AIRES, DF, ARGENTINA; MR CASTEX ACAD NACL MED, INST INVEST HEMATOL, RA-1425 BUENOS AIRES, DF, ARGENTINA; HOSP EVA PERON, RA-1650 BUENOS AIRES, DF, ARGENTINA
 CYA ARGENTINA
 SO PIGMENT CELL RESEARCH, (JUN 1995) Vol. 8, No. 3, pp. 121-131. ISSN: 0893-5785.
 DT Article; Journal
 FS LIFE
 LA ENGLISH
 REC Reference Count: 47
 ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS
 AB Two human melanoma cell lines, derived from metastases of two patients with epithelioid malignant amelanotic melanomas, and designated IIB-MEL-LES and IIB-MEL-IAN, have been established. Both cell lines have been in continuous culture over 2 years and were
 Searcher : Shears 308-4994

propagated continuously for 85 and 75 serial passages, respectively. Morphologically, IIB-MEL-LES is composed predominantly of spindle shaped cells, whereas IIB-MEL-IAN grows as a monolayer of cuboid and stellate shaped cells with many rounded cells in suspension.

Immunocytochemical studies revealed that both cell lines express S-100 **protein**, vimentin, and GD(3) and GD(2) gangliosides but are negative for keratin and collagen. Both cell lines express HLA class I and HLA-DR **antigens** in variable proportions.

The **MAGE-1** gene is expressed only by the IIB-MEL-IAN cell line, as revealed by PCR analysis. Cytogenetic analysis of both cell lines revealed abnormal karyotypes; the modal chromosome numbers of IIB-MEL-LES and IIB-MEL-IAN were 48 and 81, respectively. IIB-MEL-LES cells presented rearrangements in chromosomes 1, 14 and X, gains in chromosomes 10, 20, and 21 losses in chromosomes 15 and Y. The most frequent markers observed in IIB-MEL-IAN cells were 7q+, 10p+, 2p+, i(6p), 2q+, and 10q-. Clonal gains were observed in chromosomes 12 and 21, whereas losses were seen in chromosomes 1, 2, 3, 4, 6, 7, 11, and 17. Both cell lines were capable of forming colonies in soft agar and developed tumors when transplanted into nude mice, reproducing and maintaining the characteristics of the original tumors. These cell lines and their xenografts appear to provide useful systems for studying the biology, genetics and histogenesis of human malignant melanoma and could be utilized for the development of melanoma vaccines.

L62 ANSWER 18 OF 27 BIOSIS COPYRIGHT 1997 BIOSIS DUPLICATE 7

AN 95:487231 BIOSIS

DN 98501531

TI Expression of the MAGE gene family in human lymphocytic leukemia.

AU Schichijo S; Tsunosue R; Masuoka K; Natori H; Tamai M; Miyajima J; Sagawa K; Itoh K

CS Dep. Immunol., Kurume Univ. Sch. Med., 67-Asahi-machi, Kurume, Fukuoka 830, Japan

SO Cancer Immunology Immunotherapy 41 (2). 1995. 95-103. ISSN: 0340-7004

LA English

AB The MAGE gene family, encoding tumor-rejection **antigens** recognized by cytotoxic T lymphocytes, is frequently expressed in human solid cancers. However, its expression in leukemia has not been well studied. We have investigated MAGE gene expression at the mRNA level in human leukemia. The MAGE gene family was expressed in 17 of 34 (50%) examples of T cell leukemia (12/21 patients' peripheral blood mononuclear cells and 5/13 cell lines), in 7 of 16 (44%) cases of B cell leukemia (1/8 and 6/8 respectively), but in none of 23 myelomonocytic leukemia cases (0/16 and 0/7), as evaluated by the primers common to the **MAGE-1**, -3, -4 (-4a and/or -4b), and -6 genes and the semi-quantificative reverse transcription/polymerase chain reaction method. None of a panel of normal lymphoid cells expressed the MAGE gene family. As revealed by the primers specific for each of the MAGE genes, the **MAGE-1**, -2, -3, -4 or -6 gene was expressed in 8, 8, 6, 2, or 6 respectively out of 23 types of leukemia cell lines. Expression of the **MAGE-1 protein** in both the cell lines and patients' cells was confirmed by immunoblot analysis with the polyclonal antibody to recombinant **MAGE-1 protein**. Cellular **MAGE-4 protein** in the cell lines was measured by an enzyme-linked immunosorbent assay with the polyclonal and **monoclonal** antibodies to recombinant MAGE-4b **protein**. In summary, the MAGE gene family was found to be expressed in the substantial proportion of T cell leukemias, but in

Searcher : Shears 308-4994

no case of myelomonocytic leukemia. **Antigens** coded by the MAGE gene family could be important molecules for understanding specific immunity against lymphocytic leukemia.

L62 ANSWER 19 OF 27 MEDLINE DUPLICATE 8
 AN 95385035 MEDLINE
 TI Expression of the MAGE gene family in human lymphocytic leukemia.
 AU Shichijo S; Tsunosue R; Masuoka K; Natori H; Tamai M; Miyajima J; Sagawa K; Itoh K
 CS Department of Immunology, Kurume University School of Medicine, Fukuoka, Japan..
 SO CANCER IMMUNOLOGY, IMMUNOTHERAPY, (1995 Aug) 41 (2) 90-103.
 Journal code: CN3. ISSN: 0340-7004.
 CY GERMANY: Germany, Federal Republic of
 DT Journal; Article; (JOURNAL ARTICLE)
 LA English
 FS Priority Journals; Cancer Journals
 EM 9512
 AB The MAGE gene family, encoding tumor-rejection **antigens** recognized by cytotoxic T lymphocytes, is frequently expressed in human solid cancers. However, its expression in leukemia has not been well studied. We have investigated MAGE gene expression at the mRNA level in human leukemia. The MAGE gene family was expressed in 17 of 34 (50%) examples of T cell leukemia (12/21 patients' peripheral blood mononuclear cells and 5/13 cell lines), in 7 of 16 (44%) cases of B cell leukemia (1/8 and 6/8 respectively), but in none of 23 myelomonocytic leukemia cases (0/16 and 0/7), as evaluated by the primers common to the **MAGE-1**, -3, -4 (-4a and/or -4b), and -6 genes and the semi-quantificative reverse transcription/polymerase chain reaction method. None of a panel of normal lymphoid cells expressed the MAGE gene family. As revealed by the primers specific for each of the MAGE genes, the **MAGE-1**, -2, -3, -4 or -6 gene was expressed in 8, 8, 6, 2, or 6 respectively out of 23 types of leukemia cell lines. Expression of the **MAGE-1 protein** in both the cell lines and patients' cells was confirmed by immunoblot analysis with the polyclonal antibody to recombinant **MAGE-1 protein**. Cellular **MAGE-4 protein** in the cell lines was measured by an enzyme-linked immunosorbent assay with the polyclonal and **monoclonal** antibodies to recombinant **MAGE-4b protein**. In summary, the MAGE gene family was found to be expressed in the substantial proportion of T cell leukemias, but in no case of myelomonocytic leukemia. **Antigens** coded by the MAGE gene family could be important molecules for understanding specific immunity against lymphocytic leukemia.

L62 ANSWER 20 OF 27 BIOTECHDS COPYRIGHT 1997 DERWENT INFORMATION LTD
 AN 94-03880 BIOTECHDS
 TI Major histocompatibility complex class I and peptide antigen **monoclonal** antibody;
 application in tumor diagnosis and therapy
 PA Deut.Krebforsch.Stift.Oeffentlichen-Rechts
 PI DE 4224542 27 Jan 1994
 AI DE 92-4224542 24 Jul 1992
 PRAI DE 92-4224542 24 Jul 1992
 DT Patent
 LA German
 OS WPI: 94-035970 [05]
 AN 94-03880 BIOTECHDS

AB Production of **monoclonal** antibodies against a conjugate of a major histocompatibility complex class I molecule (I) and a **peptide antigen** (II) is effected by: (1) isolating (I); (2) inserting an (I)-encoding gene into the genome of a mouse to allow expression of the gene; (3) conjugating (I) with (II); (4) immunizing the transformed mouse with the conjugate; (5) isolating spleen cells from the mouse; and (6) producing and optionally humanizing **monoclonal** antibodies by conventional means. Also claimed are antibodies produced as above. (I) may be isolated from CS7 BL/6 mouse RMA tumor cells or human EBV transformed cells, or may be isolated from tissue, or may be produced by recombinant DNA techniques. Step (2) may be omitted if (I) is isolated from the same mouse strain as that to be immunized. (II) may be a viral or a tumor **antigen**, e.g. the human melanoma **antigen** **MAGE-1** or the tumor **antigen** produced by the HPV E6 or E7 oncogene. The **monoclonal** antibodies are useful for the diagnosis and therapy of tumors and infections, e.g. as a substitute for tumor-specific cytotoxic T-lymphocytes. (3pp)

L62 ANSWER 21 OF 27 SCISEARCH COPYRIGHT 1997 ISI (R)
 AN 95:83070 SCISEARCH
 GA The Genuine Article (R) Number: QC120
 TI IDENTIFICATION OF POTENTIAL CTL EPITOPES OF TUMOR-ASSOCIATED **ANTIGEN MAGE-1** FOR 5 COMMON HLA-A ALLELES
 AU CELIS E (Reprint); FIKES J; WENTWORTH P; SIDNEY J; SOUTHWOOD S; MAEWAL A; DELGUERCIO M F; SETTE A; LIVINGSTON B
 CS CYTEL CORP, 3525 JOHN HOPKINS COURT, SAN DIEGO, CA, 92121 (Reprint)
 CYA USA
 SO MOLECULAR IMMUNOLOGY, (DEC 1994) Vol. 31, No. 18, pp. 1423-1430. ISSN: 0161-5890.
 DT Article; Journal
 FS LIFE
 LA ENGLISH
 REC Reference Count: 28
 ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Identification of CTL epitopes for tumor-specific responses is important for the development of immunotherapies to treat cancer patients. We have developed a strategy to identify potential CTL epitopes based on screening of sequences of target **proteins** for presence of specific motifs recognized by the most common HLA-A alleles, and identification of high affinity binding **peptides** using in vitro quantitative assays. A systematic analysis using the sequence of the product of the tumor-associated **MAGE-1** gene has been carried out. All possible **peptides** of nine and ten residues, containing binding motifs for HLA-A1, -A2.1, A-3.2, -A11 and -A24 were synthesized and tested for binding using a quantitative assay. Out of 237 possible **peptide**/MHC combinations, 47 cases demonstrated good binding affinity (K-d less than or equal to 500 nM). Several **peptides** were identified as good MHC binders for each one of the five HLA-A alleles studied (five for HLA-A1, 11 for HLA-A2.1, 10 for HLA-A3.2, 16 for HLA-A11 and five for HLA-A24. Furthermore, eight of these **peptides** were found to bind well to more than one HLA-A allele. These results have important implications for the development of immunotherapeutic vaccines to treat malignant melanoma.

L62 ANSWER 22 OF 27 BIOSIS COPYRIGHT 1997 BIOSIS DUPLICATE 10
 Searcher : Shears 308-4994

AN 94:129901 BIOSIS
 DN 97142901
 TI Identification of the MAGE-1 gene product by **monoclonal** and polyclonal antibodies.
 AU Chen Y-T; Stockert E; Chen Y; Garin-Chesa P; Rettig W J; Van Der Bruggen P; Boon T; Old L J
 CS Ludwig Inst. Cancer Res., New York Unit, New York Hosp.-Cornell Med. Cent., New York, NY 10021, USA
 SO Proceedings of the National Academy of Sciences of the United States of America 91 (3). 1994. 1004-1008. ISSN: 0027-8424
 LA English
 AB The human **MAGE-1** gene encodes a melanoma **peptide antigen** recognized by autologous cytotoxic T lymphocytes. To produce antibodies against the **MAGE-1** gene product, several approaches were taken. Three oligopeptides were synthesized based on predicted **MAGE-1** amino acid sequences and were used to generate rabbit anti-**peptide** antisera. In addition, a truncated **MAGE-1** cDNA was cloned into an Escherichia coli expression vector, and recombinant **protein** was produced and purified. All three rabbit anti-**peptide** antisera showed reactivity against the immunizing **peptide**, and one reacted with the recombinant **MAGE-1 protein** by immunoblotting, but none reacted with cell lysates from **MAGE-1** mRNA-positive cells. The recombinant **MAGE-1 protein** was then used for the generation of mouse **monoclonal** and rabbit polyclonal antibodies. One IgG1 **monoclonal** antibody, MA454, as well as rabbit polyclonal antisera recognized a 46-kDa **protein** in extracts of **MAGE-1** mRNA-positive melanoma cell lines. The antibodies showed no apparent crossreactivity with products of the closely related MAGE-2 and MAGE-3 genes. Serological typing of normal and tumor cell lysates was in full agreement with mRNA analysis, showing expression of **MAGE-1 protein** in **MAGE-1** mRNA-positive testis and a subset of melanomas but not in **MAGE-1** mRNA-negative normal or tumor tissues. Transfection of the **MAGE-1** gene into a **MAGE-1** mRNA-negative melanoma cell line resulted in the expression of the 46-kDa **protein**, confirming the identity of this **protein** as the **MAGE-1** gene product.

L62 ANSWER 23 OF 27 BIOSIS COPYRIGHT 1997 BIOSIS DUPLICATE 11
 AN 94:548546 BIOSIS
 DN 98008094
 TI **MAGE-1** gene product is a cytoplasmic **protein**.
 AU Schultz-Thater E; Juretic A; Dellabona P; Luscher U; Siegrist W; Harder F; Heberer M; Zuber M; Spagnoli G C
 CS Z.L.F., Surgical Res. Lab., 20 Hebelstrasse, CH-4031 Basel, Switzerland
 SO International Journal of Cancer 59 (3). 1994. 435-439. ISSN: 0020-7136
 LA English
 AB **MAGE-1** gene encodes a human melanoma **antigen**, recognized by syngeneic cytotoxic T lymphocytes (CTL). **MAGE-1** transcripts are also detectable in breast cancers, in non-small-cell lung carcinomas and in central nervous system tumors. In order to identify, in cellular preparations, the **protein** encompassing the antigenic
 Searcher : Shears 308-4994

peptide, we generated a panel of **monoclonal** antibodies (**MABs**) against the **MAGE-1** gene product by using, as immunogen, a full-length recombinant preparation (rMAGE1), obtained through expression cloning of the relevant gene in *E. coli*. Four reagents were obtained recognizing both rMAGE-1 and the 46-kDa native **protein** in cell lines expressing **MAGE-1** mRNA. No positivity could be detected in **MAGE-1**-mRNA-negative melanoma lines. No surface labelling of **MAGE-1**-positive cell lines could be observed. In contrast, on permeabilization of MZ2 melanoma cells, all 4 **MABs** induced efficient staining, as detected by cytofluorography. Fluorescence microscopy shows that **MAGE-1** gene product is a cytoplasmic **protein** clustered in paranuclear organelle-like structures. Thus, **MAGE-1 protein** location closely resembles that of P91A and P198 murine-tumor **antigens**.

L62 ANSWER 24 OF 27 MEDLINE DUPLICATE 12
 AN 94265193 MEDLINE
 TI T cell recognition of melanoma antigens in association with HLA-A1 on allogeneic melanoma cells.
 AU Chen Q; Smith M; Nguyen T; Maher D W; Hersey P
 CS Immunology and Oncology Unit, Mater Misericordiae Hospital, Newcastle, N.S.W., Australia.
 SO CANCER IMMUNOLOGY, IMMUNOTHERAPY, (1994 Jun) 38 (6) 385-93. Journal code: CN3. ISSN: 0340-7004.
 CY GERMANY: Germany, Federal Republic of
 DT Journal; Article; (JOURNAL ARTICLE)
 LA English
 FS Priority Journals; Cancer Journals
 EM 9409
 AB Previous studies have shown that recognition of melanoma by cytotoxic T lymphocytes may be restricted by HLA-A1, A2 and other HLA **antigens**. The present study examined the cytotoxic specificity and major histocompatibility complex restriction of cloned cytotoxic T lymphocytes (CTL) isolated from a patient with the HLA phenotype A3,31 who had been immunized with a vaccine prepared from HLA-A1,3 melanoma cells. Cytotoxic assays against HLA-typed allogeneic melanoma cells indicated that cloned CTL from the patient were able to kill allogeneic melanoma cells expressing HLA-A1 but not other HLA-A1-positive cells. Studies on a representative clone indicated that proliferation and cytokine (tumour necrosis factor alpha) production in response to melanoma cells was also associated with HLA-A1 on melanoma cells. Response to the melanoma cells was associated with interleukin-4 (IL-4) rather than IL-2 production. The **antigen** recognized in the context of HLA-A1 on allogeneic melanoma cells was detected in cytotoxic assays on cells from 9 of 12 HLA-A1+ melanoma cell lines and did not appear to be the product of the **MAGE-1** or -3 genes. These findings suggest that T cells can recognize melanoma **antigens** in the context of alloantigens and that allogeneic vaccines containing "immunodominant" alloantigens may generate CTL that are ineffective against autologous melanoma. The study does not, however, exclude the possibility that CTL with specificity to the latter may be activated by allogeneic vaccines, and further studies are needed to answer this question.

L62 ANSWER 25 OF 27 JICST-EPlus COPYRIGHT 1997 JST
 AN 950162894 JICST-EPlus
 TI Preparatino of **monoclonal** antibody against **MAGE-**
 Searcher : Shears 308-4994

1 protein and detection of this antigen
in cancer cells.

- AU SHICHIJO SHIGEKI; TAKAHASHI KOICHI; TSUNOSUE RIKA; HARA AKINORI;
TAKASU HIDEO; SAKATA MOTOKO; TANAKA YASUYUKI; HAYASHI AKIHIRO; ITO
KYOGO
- CS Kurume Univ.
- SO Nippon Men'eki Gakkai Sokai, Gakujutsu Shukai Kiroku, (1994) vol.
24, pp. 110. Journal Code: Z0383B
- CY Japan
- LA Japanese
- STA New
-
- L62 ANSWER 26 OF 27 MEDLINE DUPLICATE 13
- AN 93208203 MEDLINE
- TI Disseminated melanoma, preclinical therapeutic studies, clinical
trials, and patient treatment.
- AU Lejeune F; Bauer J; Leyvraz S; Lienard D
- CS Centre Pluridisciplinaire d'Oncologie (CPO), University of Lausanne,
Switzerland..
- SO CURRENT OPINION IN ONCOLOGY, (1993 Mar) 5 (2) 390-6. Ref: 46
Journal code: A1V. ISSN: 1040-8746.
- CY United States
- DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
- LA English
- FS Priority Journals
- EM 9307
- AB Disseminated malignant melanoma is a very resistant tumor to
therapy. Mechanisms of resistance to chemotherapy may be due to
glutathione reductase and O6 alkyltransferase, two enzymes
especially able to detoxify from alkylation. An interesting model is
represented by dacarbazine in the treatment of melanoma with
nitrosourea derivatives. Cytokines may come to play an increasing
role in the combination with chemotherapy; interferon-alpha and
interleukin-2, for example, seem to potentiate the action of
chemotherapy in well-designed clinical protocols. Moreover, tumor
necrosis factor-alpha was shown to be active in combination therapy
with interferon-gamma and chemotherapy when administered by
isolation perfusion. Targeting with **monoclonal** antibodies
or melanocyte-stimulating hormone-alpha conjugated to cytotoxic
agents represents a promising area. The discovery of a gene,
designated **MAGE1**, coding for a **peptide** presented
by HLA-A1 and able to specifically activate cytotoxic T lymphocytes
may represent a unique approach to specific active immunotherapy for
melanoma. The interference with integrins and adhesion molecules may
play a role in the prevention of metastases. Some preclinical models
seem to validate this approach. Current treatment of disseminated
malignant melanoma involves chemotherapy often associated with other
cytotoxic agents or cytokines, which may potentiate the antitumor
effect. Other therapeutic issues reviewed concern targeting and
immunotherapy. This review ends with a survey of biologic factors
that may constitute new approaches to melanoma therapy.
-
- L62 ANSWER 27 OF 27 EMBASE COPYRIGHT 1997 ELSEVIER SCI. B.V.
- AN 93111783 EMBASE
- TI Immunologic recognition of malignant melanoma by autologous T
lymphocytes.
- AU Carrel S.; Johnson J.P.
- CS Lausanne Branch, Ludwig Institute for Cancer Research, Ch des
Searcher : Shears 308-4994

08/560024

SO Boveresses 155, CH 1066 Epalinges, Switzerland
CURR. OPIN. ONCOL., (1993) 5/2 (383-389).
ISSN: 1040-8746 CODEN: CUOOE8
CY United States
DT Journal
FS 016 Cancer
LA English
SL English
AB T lymphocytes specifically recognizing autologous tumor cells in vitro can be generated from melanoma patients. Recognition of tumor cells by both CD4 and CD8 lymphocytes is mediated through the T-cell receptor and is restricted by HLA **antigens**. Although HLA-A2 has been identified as a restricting allele for many melanoma-specific cytotoxic T lymphocytes, T cells directed against **antigens** unique to each patient's tumor as well as **antigens** common to melanomas from unrelated individuals can be restricted by several different HLA alleles. A common melanoma **antigen** recognized in association with HLA-A1 has now been identified. The **antigen** is a nonapeptide derived from the gene **MAGE1**, a normal cellular gene preferentially expressed in a variety of solid tumors. Melanoma cells have been found to produce a soluble form of the intercellular adhesion molecule-1. Soluble intercellular adhesion molecule-1 effectively inhibits cell-mediated cytotoxicity in vitro, raising the possibility that its expression in vivo could promote escape of the tumor cells from immune effectors.

FILE 'USPATFULL' ENTERED AT 10:44:25 ON 03 APR 1997
CA INDEXING COPYRIGHT (C) 1997 AMERICAN CHEMICAL SOCIETY (ACS)

FILE COVERS 1971 TO PATENT PUBLICATION DATE: 1 Apr 1997 (19970401/PD)
FILE LAST UPDATED: 2 Apr 1997 (970402/ED)
HIGHEST PATENT NUMBER: US5617579
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ISSUE CLASS FIELDS (/INCL) CURRENT THROUGH: 1 Apr 1997 (19970401/PD)
REVISED CLASS FIELDS (/NCL) CURRENT THROUGH: FEB 1997
USPTO MANUAL OF CLASSIFICATIONS THESAURUS ISSUE DATE: DEC 1996

>>> Page images are available for patents from 1/1/94. Current <<<
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>>> fields. This thesaurus includes catchword terms from the <<<
>>> USPTO/MOC subject headings and subheadings. Thesauri are also <<<
>>> available for the WIPO International Patent Classification <<<
>>> (IPC) Manuals, editions 1-6, in the /IC1, /IC2, /IC3, /IC4, <<<
>>> /IC5, and /IC (/IC6) fields, respectively. The thesauri in <<<
>>> the /IC5 and /IC fields include the corresponding catchword <<<
>>> terms from the IPC subject headings and subheadings. <<<

This file contains CAS Registry Numbers for easy and accurate substance identification.

2134119 1
 1155544 I
 1 MAGE1
 0 MAGEI
 13260 POLYPEPTIDE#
 243 POLYPROTEIN#
 62831 PROTEIN#
 22013 PEPTIDE#
 17596 ANTIGEN#
 16 L37(L) (POLYPEPTIDE# OR POLYPROTEIN# OR PROTEIN# OR PEPTIDE
 # OR ANTIGEN#)
 166 MOAB#
 1948 MAB#
 9386 MONOCLON?
 4038 HYBRIDOM?
 L63 9 L49 AND (MOAB# OR MAB# OR MONOCLON? OR HYBRIDOM?)

=> d 1-9 bib abs; fil hom

L63 ANSWER 1 OF 9 USPATFULL
 AN 97:22645 USPATFULL
 TI Isolated nucleic acid molecules useful in determining expression
 of a tumor rejection antigen precursor
 IN De Plaen, Etienne, Brussels, Belgium
 Boon-Falleur, Thierry, Brussels, Belgium
 Lethe, Bernard, Brussels, Belgium
 Szikora, Jean-Pierre, Brussels, Belgium
 De Smet, Charles, Brussels, Belgium
 Chomez, Patrick, Brussels, Belgium
 PA Ludwig Institute for Cancer Research, New York, NY, United States
 (U.S. corporation)
 PI US 5612201 970318
 AI US 94-299849 940901 (8)
 RLI Continuation-in-part of Ser. No. US 93-37230, filed on 26 Mar 1993
 which is a continuation-in-part of Ser. No. US 91-807043, filed on
 12 Dec 1991, now patented, Pat. No. US 5342774 which is a
 continuation-in-part of Ser. No. US 91-764364, filed on 23 Sep
 1991, now patented, Pat. No. US 5327252 which is a
 continuation-in-part of Ser. No. US 91-728838, filed on 9 Jul
 1991, now abandoned which is a continuation-in-part of Ser. No. US
 91-705702, filed on 23 May 1991, now abandoned
 DT Utility
 EXNAM Primary Examiner: Zitomer, Stephanie W.; Assistant Examiner: Rees,
 Dianne
 LREP Felte & Lynch
 CLMN Number of Claims: 3
 ECL Exemplary Claim: 3
 DRWN 23 Drawing Figure(s); 19 Drawing Page(s)
 LN.CNT 2550
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.
 AB The invention relates to nucleic acid molecules which are useful
 in determining expression of the family of molecules known as the
 MAGE tumor rejection antigen precursors. These nucleic acid are
 molecules useful as diagnostic aids for determining whether or not
 an individual has cancer. Methods using these molecules are also
 described.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L63 ANSWER 2 OF 9 USPATFULL

Searcher : Shears 308-4994

08/560024

AN 97:16085 USPATFULL
TI Compositions and methods for treating and preventing pathologies including cancer
IN Samid, Dvorit, Rockville, MD, United States
PA The United States of America as represented by the Department of Health and Human Services, Washington, DC, United States (U.S. government)
PI US 5605930 970225
AI US 94-207521 940307 (8)
RLI Continuation-in-part of Ser. No. US 93-135661, filed on 12 Oct 1993 which is a continuation-in-part of Ser. No. US 91-779744, filed on 21 Oct 1991
DT Utility
EXNAM Primary Examiner: Nutter, Nathan M.
LREP Needle & Rosenberg, P.C.
CLMN Number of Claims: 25
ECL Exemplary Claim: 1
DRWN 60 Drawing Figure(s); 43 Drawing Page(s)
LN.CNT 7722
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Compositions and methods of treating anemia, cancer, AIDS, or severe .beta.-chain hemoglobinopathies by administering a therapeutically effective amount of phenylacetate or pharmaceutically acceptable derivatives thereof or derivatives thereof alone or in combination or in conjunction with other therapeutic agents including retinoids, hydroxyurea, and flavonoids. Intravesicle methods of treatment of cancers phenylacetate. Pharmacologically-acceptable salts alone or in combinations and methods of preventing AIDS and malignant conditions, and inducing cell differentiation are also aspects of this invention. A product as a combined preparation of phenylacetate and a retinoid, hydroxyurea, or flavonid (or other mevalonate pathway inhibitor) for simultaneous, separate, or sequential use in treating a neoplastic condition in a subject. Methods of modulating lipid metabolism and/or reducing serum triglycerides in a subject using phenylacetate.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L63 ANSWER 3 OF 9 USPATFULL
AN 97:1165 USPATFULL
TI Isolated, MAGE-3 derived peptides which complex with HLA-A2 molecules and uses thereof
IN Townsend, Alan, Headington, England
Bastin, Judy, Headington, England
Boon-Falleur, Thierry, Brussels, Belgium
van der Bruggen, Pierre, Brussels, Belgium
Coulie, Pierre, Brussels, Belgium
Gajewski, Thomas, Brussels, Belgium
PA Ludwig Institute for Cancer Research, New York, NY, United States (U.S. corporation)
The Chancellor, Masters and Scholars of the University of Oxford, Oxford, England (non-U.S. corporation)
PI US 5591430 970107
AI US 94-261160 940617 (8)
RLI Continuation-in-part of Ser. No. US 94-217186, filed on 24 Mar 1994, now patented, Pat. No. US 5585461
DT Utility
EXNAM Primary Examiner: Cunningham, Thomas M.
LREP Felfe & Lynch

Searcher : Shears 308-4994

CLMN Number of Claims: 6
 ECL Exemplary Claim: 1,3
 DRWN 15 Drawing Figure(s); 9 Drawing Page(s)
 LN.CNT 692

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB Tumor rejection antigens derived from tumor rejection precursor MAGE-3 have been identified. These "TRAS" bind to the MHC-class I molecule HLA-A2, and the resulting complexes stimulate the production of cytolytic T cell clones which lyse the presenting cells. The peptides and complexes may be used diagnostically, therapeutically, and as immunogens for the production of antibodies, or as targets for the generation of cytolytic T cell clones.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L63 ANSWER 4 OF 9 USPATFULL

AN 96:118503 USPATFULL
 TI Isolated nucleic acid molecules which are members of the MAGE-Xp family and uses thereof
 IN Lurquin, Christophe, Brussels, Belgium
 Boon-Falleur, Thierry, Brussels, Belgium
 PA Ludwig Institute for Cancer Research, New York, NY, United States (U.S. corporation)
 PI US 5587289 961224
 AI US 95-403388 950314 (8)
 DT Utility
 EXNAM Primary Examiner: Jones, W. Gary; Assistant Examiner: Atzel, Amy
 LREP Felfe & Lynch
 CLMN Number of Claims: 12
 ECL Exemplary Claim: 1,9
 DRWN No Drawings
 LN.CNT 547

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The invention relates to members of the MAGE-Xp family of nucleic acid molecules. These molecules differ from the previously described MAGE nucleic acid molecules in that members of the MAGE-Xp family do not hybridize to the previously identified MAGE sequences. Further, the members of the MAGE-Xp family are found on the Xp arm of the X chromosome rather than on the Xq chromosome, as was the case with the previously identified MAGE genes.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L63 ANSWER 5 OF 9 USPATFULL

AN 96:116468 USPATFULL
 TI Isolated, MAGE-3 derived peptides which complex with HLA-A2 molecules and uses thereof
 IN Townsend, Alan, Headington, England
 Bastin, Judy, Headington, England
 Boon-Falleur, Thierry, Brussels, Belgium
 van der Bruggen, Pierre, Brussels, Belgium
 Coulie, Pierre, Brussels, Belgium
 PA Ludwig Institute for Cancer Research, New York, NY, United States (U.S. corporation)
 The Chancellor, Masters and Scholars of the University of Oxford, Oxford, United Kingdom (non-U.S. corporation)
 PI US 5585461 961217
 AI US 94-217186 940324 (8)
 DT Utility

Searcher : Shears 308-4994

EXNAM Primary Examiner: Cunningham, Thomas M.

LREP Felfe & Lynch

CLMN Number of Claims: 4

ECL Exemplary Claim: 1

DRWN 2 Drawing Figure(s); 2 Drawing Page(s)

LN.CNT 440

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB Tumor rejection antigens derived from tumor rejection precursor MAGE-3 have been identified. These "TRAS" bind to the MHC-class I molecule HLA-A2, and the resulting complexes stimulate the production of cytolytic T cell clones which lyse the presenting cells. The peptides and complexes may be used diagnostically, therapeutically, and as immunogens for the production of antibodies, or as targets for the generation of cytolytic T cell clones.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L63 ANSWER 6 OF 9 USPATFULL

AN 96:82795 USPATFULL

TI Isolated tumor rejection antigen precursor MAGE-2 derived peptides, and uses thereof

IN Melief, Cornelis J. M., Leiden, Netherlands

Visseren, M. J. W., Leiden, Netherlands

Kast, W. M., Leiden, Netherlands

van der Bruggen, Pierre, Brussels, Belgium

Boon-Falleur, Thierry, Brussels, Belgium

PA University of Leiden, Leiden, Netherlands (non-U.S. corporation)

PI US 5554724 960910

AI US 94-217188 940324 (8)

DT Utility

EXNAM Primary Examiner: Cunningham, Thomas M.

LREP Felfe & Lynch

CLMN Number of Claims: 4

ECL Exemplary Claim: 1

DRWN 2 Drawing Figure(s); 1 Drawing Page(s)

LN.CNT 891

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The invention describes peptides derived from tumor rejection antigen precursor MAGE-2. These peptides bind with HLA-A2 molecules, thus presenting complexes which provoke cytolytic T cell production. The resulting "CTLs" are specific for complexes of HLA-A2 and the peptide. The complexes can be used to generate **monoclonal** antibodies. The cytolytic T cells produced may be used in the context of immunotherapy, such as adoptive transfer.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L63 ANSWER 7 OF 9 USPATFULL

AN 96:82581 USPATFULL

TI Isolated, MAGE-3 derived peptides which complex with HLA-A2 molecules and uses thereof

IN van der Bruggen, Pierre, Brussels, Belgium

Boon-Falleur, Thierry, Brussels, Belgium

Traversari, Catia, Milan, Italy

Fleischauer, Katharina, Milan, Italy

PA Ludwig Institute For Cancer Research, New York, NY, United States (U.S. corporation)

PI US 5554506 960910

Searcher : Shears 308-4994

AI US 94-217187 940324 (8)
 DT Utility
 EXNAM Primary Examiner: Cunningham, Thomas M.
 LREP Felfe & Lynch
 CLMN Number of Claims: 3
 ECL Exemplary Claim: 3
 DRWN No Drawings
 LN.CNT 419

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB Tumor rejection antigens derived from tumor rejection precursor MAGE-3 have been identified. These "TRAS" bind to the MHC-class I molecule HLA-A2, and the resulting complexes stimulate the production of cytolytic T cell clones which lyse the presenting cells. The peptides and complexes may be used diagnostically, therapeutically, and as immunogens for the production of antibodies, or as targets for the generation of cytolytic T cell clones.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L63 ANSWER 8 OF 9 USPATFULL

AN 96:67925 USPATFULL

TI **Monoclonal** antibodies which bind to tumor rejection **antigen precursor mage-1**

IN Chen, Yao-Tseng, New York, NY, United States
 Stockert, Elisabeth, New York, NY, United States
 Chen, Yachi, New York, NY, United States
 Garin-Chesa, Pilar, Biberach, Germany, Federal Republic of
 Rettig, Wolfgang J., Biberach, Germany, Federal Republic of
 van der Bruggen, Pierre, Brussels, Belgium
 Boon-Falleur, Thierry, Brussels, Belgium
 Old, Lloyd J., New York, NY, United States
 PA Ludwig Institute for Cancer Research, New York, NY, United States
 (U.S. corporation)
 Cornell Research Foundation, Inc., Ithaca, NY, United States (U.S. corporation)

PI US 5541104 960730

AI US 94-190411 940201 (8)

RLI Continuation-in-part of Ser. No. US 93-37230, filed on 26 Mar 1993 which is a continuation-in-part of Ser. No. US 91-807043, filed on 12 Dec 1991, now patented, Pat. No. US 5342774 which is a continuation-in-part of Ser. No. US 91-764365, filed on 23 Sep 1991, now abandoned which is a continuation-in-part of Ser. No. US 91-728838, filed on 9 Jul 1991, now abandoned which is a continuation-in-part of Ser. No. US 91-705702, filed on 23 May 1991, now abandoned

DT Utility

EXNAM Primary Examiner: Budens, Robert C.; Assistant Examiner: Nisbet, T. Michael

LREP Felfe & Lynch

CLMN Number of Claims: 4

ECL Exemplary Claim: 1

DRWN 9 Drawing Figure(s); 5 Drawing Page(s)

LN.CNT 556

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The invention relates to **monoclonal** antibodies which specifically bind to the tumor rejection **antigen precursor molecule MAGE-1, hybridomas** which produce these **monoclonal** antibodies, and their use. Also described is a recombinant form of **MAGE-**
 Searcher : Shears 308-4994

08/560024

1, **peptides** which are useful as immunogens, and immunogenic compositions containing the **peptides** and an adjuvant.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L63 ANSWER 9 OF 9 USPATFULL

AN 94:75456 USPATFULL

TI Nucleotide sequence encoding the tumor rejection **antigen** precursor, **MAGE-1**

IN Boon, Thierry, Brussels, Belgium
van der Bruggen, Pierre, Brussels, Belgium
Van den Eynde, Benoit, Brussels, Belgium
Van Pel, Aline, Brussels, Belgium
De Plaen, Etienne, Brussels, Belgium
Lurquin, Christophe, Brussels, Belgium
Chomez, Patrick, Brussels, Belgium
Traversari, Catia, Milan, Italy

PA Ludwig Institute for Cancer Research, New York, NY, United States (U.S. corporation)

PI US 5342774 940830

AI US 91-807043 911212 (7)

RLI Continuation-in-part of Ser. No. US 91-764364, filed on 23 Sep 1991, now abandoned which is a continuation-in-part of Ser. No. US 91-728838, filed on 9 Jul 1991, now abandoned which is a continuation-in-part of Ser. No. US 91-705702, filed on 23 May 1991, now abandoned

DT Utility

EXNAM Primary Examiner: Ellis, Joan

LREP Felfe & Lynch

CLMN Number of Claims: 18

ECL Exemplary Claim: 1,11,12

DRWN 33 Drawing Figure(s); 32 Drawing Page(s)

LN.CNT 1836

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The invention relates to an isolated DNA sequence which codes for an antigen expressed by tumor cells which is recognized by cytotoxic T cells, leading to lysis of the tumor which expresses it. Also described are cells transfected by the DNA sequence, and various therapeutic and diagnostic uses arising out of the properties of the DNA and the antigen for which it codes.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

FILE 'HOME' ENTERED AT 10:48:58 ON 03 APR 1997

MAPELH (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsrch_ntp n.a. - n.a. Smith-Waterman search, using a protein database
which has been backtranslated into n.a. using IUPAC symbols

Run on: Thu Apr 3 12:05:37 1997; MasPar time 52.93 Seconds
Tabular output not generated. 969.921 Million cell updates/sec

Title: >US-08-190-411A-1
Description: (3931-4761) from 5841104.seq
Perfect Score: 4155
N.A. Sequence: 3931 GCCCAACAGAGCCCTGG.....CAAGAGTTCGCTTTTCTTC 4761
Comp: CCGGTTCTTCTCCGGACC.....GTTCAAGCGAAAGAAAG

Scoring table: TABLE bktranslate2
Gap 30

Nmatch STD : Dbase 0; Query 0

Searched: 88003 seqs, 30886968 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq25
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18

Statistics: Mean 55.371; Variance 240.978; scale 0.230

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	3176	76.4	309	13	R70909 Human melanoma antige	3.17e-287
2	191	4.6	16	15	R82216 HLA-C-clone 10 derive	1.54e-03
3	154	3.7	14	15	R80618 Immunogenic peptide o	6.62e-01
c 4	149	3.6	158	4	R22766 HPV E6 peptide.	1.44e+00

1-4

c 5	149	3.6	188	12	R63865	HPV16 E6/E7 proteins.	1.44e+00
c 6	149	3.6	263	5	R27725	HPV 16 E6 protein fra	1.44e+00
c 7	146	3.5	12	15	R80620	Immunogenic peptide o	2.28e+00
c 8	141	3.4	12	15	R82217	HLA-C-clone 10 derive	4.86e+00
c 9	141	3.4	12	15	R80619	Immunogenic peptide o	4.86e+00
c 10	139	3.3	149	8	R40919	HPV E6 region product	6.56e+00
c 11	135	3.2	10	13	R70952	Human melanoma antige	1.19e+01
c 12	135	3.2	351	4	R24393	Sequence of Histidine	1.19e+01
c 13	135	3.2	1529	18	R97985	CORC potassium channe	1.19e+01
c 14	130	3.1	10	9	R49203	HLA-A1 MAGE 1 antigen	2.45e+01
c 15	127	3.1	10	9	R47327	HLA-A3 MAGE 1 antigen	3.77e+01
c 16	126	3.0	10	9	R47331	HLA-A3 MAGE 1 antigen	4.34e+01
c 17	126	3.0	10	13	R70946	Human melanoma antige	4.34e+01
c 18	126	3.0	10	13	R70958	Human melanoma antige	4.34e+01
c 19	126	3.0	10	9	R47332	HLA-A1 MAGE 1 antigen	4.34e+01
c 20	125	3.0	10	13	R65124	MAGE 1 immunogenic pe	5.00e+01
c 21	125	3.0	10	9	R49201	HLA-A3 MAGE 1 antigen	5.00e+01
c 22	125	3.0	11	12	R73823	Antigen fragment 139,	5.00e+01
c 23	125	3.0	11	16	R80899	MAGE-2 peptide (resid	5.00e+01
c 24	124	3.0	108	7	R35721	Tryptophan aporepress	5.75e+01
c 25	123	3.0	108	7	R35714	Tryptophan aporepress	6.61e+01
c 26	123	3.0	540	15	R76062	Protein kinase PKC be	6.61e+01
c 27	120	2.9	9	13	R70947	Human melanoma antige	1.00e+02
c 28	121	2.9	10	15	R78912	MAGE 1 200-209 cyto	8.73e+01
c 29	121	2.9	10	13	R70941	Human melanoma antige	8.73e+01
c 30	121	2.9	10	13	R70955	Human melanoma antige	8.73e+01
c 31	121	2.9	10	12	R73824	Antigen fragment 140,	8.73e+01
c 32	121	2.9	10	9	R47333	HLA-A1 MAGE 1 antigen	8.73e+01
c 33	121	2.9	10	13	R70956	Human melanoma antige	8.73e+01
c 34	121	2.9	10	13	R70964	Human melanoma antige	8.73e+01
c 35	121	2.9	11	12	R73836	Antigen fragment 152,	8.73e+01
c 36	121	2.9	11	16	R80934	MAGE-2 peptide (resid	8.73e+01
c 37	122	2.9	51	3	R13365	P2302 HCV antigen (23	7.60e+01
c 38	122	2.9	51	7	R33884	Polyptide p2302 com	7.60e+01
c 39	121	2.9	543	1	R24022	Human promyelo-leukae	8.73e+01
c 40	121	2.9	647	10	R48975	Human betai, 6-N-acety	8.73e+01
c 41	121	2.9	740	9	R47174	Predicted sequence of	8.73e+01
c 42	121	2.9	856	10	R51249	FIV PET-Fl4 envelope	8.73e+01
c 43	121	2.9	856	10	R51248	FIV petaluma envelope	8.73e+01
c 44	120	2.9	1529	18	R97985	CORC potassium channe	1.00e+02
c 45	121	2.9	3054	8	R40841	Translation of TEV la	8.73e+01

ALIGNMENTS

RESULT 1

ID R70909 standard; Protein; 309 AA.
AC R70909;
DT 09-OCT-1995 (first entry)
DE Human melanoma antigen MAGE-1.
KW Human melanoma antigen; MAGE-1; vaccines; MAGE associated tumours;
KW HLA-restricted cytotoxic T-lymphocyte activity.
OS Homo sapiens.
PN W09504542-A.
PD 16-FEB-1995.
PF 02-AUG-1994; U08721.
PR 06-AUG-1993; US-103623.
PA (CYTE-) CYTEL CORP.
PI Fikes JD, Livingston BD, Sette AD, Sidney JC;
DR WPI; 95-090681/12.

Query Match 4.6%; Score 191; DB 15; Length 16;
Best Local Similarity 55.3%; Pred. No. 1.54e-03;
Matches 26; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

RESULT 3
ID R80618 standard: protein: 14 AA.

PF	05-JAN-1995; U00095.
PR	01-FEB-1994; US-190411.
PA	(LUDW-) LUDWIG INST CANCER RES.
PA	(SLOK) SLOAN KETTERING INST CANCER RES.
PA	(SLOK) MEMORIAL SLOAN-KETTERING CANCER CENT.
PI	Boon-falleur T, Chen Y, Garin-chesa P, Old Lu, Rettig WJ;
PI	Stockert E, Van der bruggen P;
PI	WPI; 95-283606/37.
PR	New monoclonal antibody binding specifically to MAGE-1 - useful for
PT	diagnosis and monitoring of cancer, also new hybridomas, recombinant
PT	MAGE-1 and immunogenic peptide(s)
PT	Claim 12; Page 20; 33pp; English.
PS	A monoclonal antibody directed against the tumour rejection antigen
CC	(MAGE-1) can be used to detect MAGE-1 in samples by standard
CC	immunoassay methods for diagnosis and monitoring of cancer etc. The
CC	monoclonal antibody is designated MA454 and is produced by the
CC	hybridoma deposited as ATCC HB11540. The monoclonal antibody is
CC	specific for MAGE-1, having no reactivity for MAGE-2 or MAGE-3.
CC	Peptide fragments of MAGE-1 (See R80618-20) may be useful as
CC	immunogens for production of the monoclonal antibody and antisera.
CC	Sequence 14 AA;
SO	

Query Match 3.7%; Score 154; DB 15; Length 14;
Best Local Similarity 48.8%; Pred. No. 6.62e-01;
Matches 20; Conservative 14; Mismatches 7; Indels 0; Gaps 0;

RESULT	4
ID	R22766 standard; peptide; 158 AA.
AC	R22766;
DT	21-SEP-1992 (first entry)
DE	HPV E6 peptide.
KW	Human: papillomavirus: immunogenic; warts; carcinoma;

RESULT	4
ID	B22766
standard:	peptide; 158 AA;

DT 21-SEP-1992 (first entry)

KW Human; papillomavirus; immunogenic

OS Synthetic.

PN W09205248-A.

26-SEP-1991; 00/08L.
PF

PA (BRIM) BRISTOL-MYERS SQUIB.

FI THOMAS E A.
DD FBI: 02-132110/16

FI and recombinant cells encoding the immunogenic peptide(s), derived from

propylaxis or survival rates
infection
PT

The peptide is the sequence of the

regions) of HPV 16 E6 were synthesized

148-158. Compositions contg. the

CC genic peptides may be utilised in

CC prevention or retardation of cerv

CC See also R22767.

Model	Best Local Similarity	Pred.
Model 1	34.3%	5.5

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DE 213 artggytnaarttytaywsnaaratnws

CP 4293 AGTGGCTGGTAAATTTTGAAGACACACCTC

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DC ZVS gnaicracny ciugai calcal ca ya aa ya ac

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RESULT      5
IID      R63865 standard; Protein; 188 AA.
AC      R63865;
28-JUN-1995 (first entry)
DE      HPV16 E6/E7 proteins.
KW      HPV; HPV16; E6 protein; E7 protein; diagnosis; cervical dysplasia;
KW      cervix cancer.
OS      Human papillomavirus strain 16.
FH      Location/Qualifiers
FT      Protein
FT      1..158
FT      /label= E6_protein
FT      Protein
FT      159..188
FT      /label= E7_protein
FT      Protein
FT      W09426934-A.
FT      24-NOV-1994.
PF      06-MAY-1994; U05085.
PF      06-MAY-1994; U8-058920.
PP      (BAXT ) BAXTER DIAGNOSTICS INC.
PI      Brown JT;
PI      WPI; 95-006821/01.
DR      P-PSDB; Q75470.
DPT      Human papilloma virus detection assay - by amplification using
PPT      self sustained sequence replication and hybridisation with a
PT      detector probe
PT      Disclosure; Page 24-26; 79pp; English.
CC      The sequences of the E6 and E7 polypeptide-encoding regions of human
CC      papillomavirus (HPV) 16 and 18 are given in Q75470-71 and the
CC      encoded proteins in R63865-66, respectively. Probes and primers
CC      based on these sequences were used for HPV infection diagnosis;
CC      expression of E6 and E7 is diagnostic for cervical cancer or pre-
CC      malignant states.
CC      Sequence 188 AA.
SO

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Query Match	3.6%	Score 149;	DB 12;	Length 188;
Best Local Similarity	34.3%;	Ref. No. 1.44e+00;		
Matches	37;	Conservative	29;	Mismatches 41;
			Indels	1;
			Gaps	1;

Db	C	l	k	f	y	s	k	i	s	e	y	r	h	y	c	y	s	l	y	g
Dc	215	artgyvnaart	tyt	yawna	rathw	ngartay	mgncay	tayt	gtyaw	smnyntay	g	274								
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Cp	4295	AGTCCTGTA	TTTGTAT	GATGAC	ATCTCC	-AGCA	TTTTC	GTGCTT	TGTG	ACTGCT	CCCTG	4237								
Ct		C	L	*	F	L	M	T	L	S	x	H	F	C	L	C	D	W	L	
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Db	275	gnacnaeny	ngarc	arcartay	aa	yaarc	cnyn	tntg	tyg	aytynt	na	322								
Dc																				
Cp	4236	GCTCGAT	TATTGT	GAGGAC	GA	AAAC	CAAC	CAAT	CAGC	CACTTCT	TA	4189								
Ct		S	I	F	E	E	Q	K	T	N	Q	I	S	H	L	L				

RESULT	6
ID	R27725 standard; Protein; 263 AA.
AC	R27725;
DE	09-MAR-1993 (first entry)
DT	HPV 16 E6 protein fragment.
DE	Virus vector; vaccinia virus; papillomavirus; HPV; human;
KW	amplification; immunotherapeutic.
OS	Human papillomavirus 16.
Key	Location/Qualifiers
FT	Peptide 1..159

FT /note= "HPV-16 E6 protein"
PN WO9216636-A.
PD 01-OCT-1992.
PF 10-MAR-1992; G000424.
PR 14-MAR-1991; GB-005383.
PA (IMMUNOLOGY LTD.
PI Bournsall MEG, Inglis SC, Munro AJ;
DR WPI; 92-349219/42.
DR N-PDSB; Q29389.
PT Recombinant virus vectors encoding human papillomavirus proteins
PT - for treating and vaccinating against HPV infections and
PT conditions caused by them, such as cervical cancer
PT Disclosure; Fig 1a; 83pp; English.
PS The fragment of DNA contg. the HPV-16 E6/E7 coding region was
CC prep'd. by PCR from plasmid pBR322/HPV16 (Durst et al., PNAS, 80:
CC 3812 (1983)) using oligonucleotides S05 and S06. The prod. of the
CC third reading frame is the HPV-16 E6 protein whereas the second
CC reading frame encodes HPV-16 E7. The E6 and E7 ORFs are fused
CC together to form a single continuous ORF via site directed mutagenesis
CC and the immortalising potential of E7 is removed by altering two key
CC codons of the HPV E7 sequence. The single ORF of HPV-16 E6/E7 may be
CC inserted into vaccinia virus DNA at neutral sites (pref. by inserting
CC two sets of the DNA in opposite orientations to overcome the problem
CC of intertypic recombination) to make a recombinant virus vector for
CC use immunotherapeutically to activate cells of the immune system
CC against HPV. See also R27/23-43.
CC Sequence 263 AA;
SQ

	Query Match	3.6%	Score 149;	DB 5;	Length 263;																
	Best Local Similarity	34.3%;	Pred. No. 1.44e+00;																		
	Matches	37;	Conservative	29;	Mismatches 41; Indels 1; Gaps 1;																
Ddb	C	l	k	f	y	s	k	i	s	e	y	r	h	y	c	y	s	l	y	g	
Ddc	218	artgyvnaartiyta	wnaarathwsgartaymgncayta	tytgvtaywsnyntayg	277																
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Cp	4295	AGTGGTCTGAATTTGATGACACTTCG	-ACGACTTTGCGCTTTGACGTGCTCGCTG	4237																	
Ct		C	L	*	F	L	M	T	L	S	x	H	F	C	L	C	D	W	L	P	G
Ddb		t	t	l	e	q	q	y	n	k	p	l	c	d	l	l					
Ddc	278	gnacnaeyntngarc	cartayaa	yaarccnyntatg	vgayyyntayna	325															
Cp		:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	
Ct	4236	GCTGATTTTGTAGGAGCAACCAACCA	CCACCAATCATGCGACTCTCTTA	4189																	
Ddb		S	I	F	E	E	Q	K	T	N	Q	I	S	H	L	L					

RESULT	7
ID	R80620 standard; Protein; 12 AA.
AC	R80620;
DE	28-FEB-1996 (first entry)
DT	Immunogenic peptide of tumour rejection antigen (MAGE-1).
DD	Tumour rejection antigen; MAGE-1; monoclonal antibody; Mab;
KK	diagnosis; immunoassay; cancer; immunogen; antisera.
KK	Homo sapiens.
OW	W09520974-A1.
PN	PD 10-AUG-1995.
PD	PD 05-JAN-1995; U00095.
PF	01-FEB-1994; US-190411.
PR	(LUDW-) LUDWIG INST CANCER RES.
PA	(SLOK) SLOAN KETTERING INST CANCER RES.
PA	(SLOK) MEMORIAL SLOAN-KETTERING CANCER CENT.

PI Boon-falleur T, Chen Y, Garin-chesa P, Old LJ, Rettig WJ;
 PI Stockert E, Van der bruggen P;
 DR WPI; 95-283606/37.
 PT New monoclonal antibody binding specifically to MAGE-1 - useful for
 PT diagnosis and monitoring of cancer, also new hybridomas, recombinant
 PT MAGE-1 and immunogenic peptide(s)
 PS Claim 12; Page 20; 33pp; English.
 CC A monoclonal antibody directed against the tumour rejection antigen
 CC (MAGE-1) can be used to detect MAGE-1 in samples by standard
 CC immunoassay methods for diagnosis and monitoring of cancer etc. The
 CC monoclonal antibody is designated MA454 and is produced by the
 CC hybridoma deposited as ATCC HB11540. The monoclonal antibody is
 CC specific for MAGE-1, having no reactivity for MAGE-2 or MAGE-3.
 CC Peptide fragments of MAGE-1 (See R80618-20) may be useful as
 CC immunogens for production of the monoclonal antibody and antisera.
 SQ Sequence 12 AA;

Query Match 3.5%; Score 146; DB 15; Length 12;
 Best Local Similarity 61.1%; Pred. No. 2.28e+00;
 Matches 22; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

Db d v k e a d p t g h s y
 Dt 1 gavgtnaargarcngayccnagcngcaywantay 36
 Qy 4352 GAGCTGAGGAGCAGACCCCGCCGCACTCTAT 4387
 Qt D V K E A D P T G H S Y

RESULT 8
 ID R82217 standard; peptide; 12 AA.
 AC R82217;
 DT 18-MAR-1996 (first entry)
 DE HLA-C-clone 10 derived peptide.
 KW HLA; cellular disorder; melanoma; diagnosis; identification; T cell;
 KW cytotoxic; immune response.
 OS Homo sapiens.
 PN W09521630-A1.
 PD 17-AUG-1995.
 PF 26-JAN-1995; U01446.
 PR 14-FEB-1994; US-195186.
 PR 15-FEB-1994; US-196630.
 PR 18-AUG-1994; US-292492.
 PA (LUDW-) LUDWIG INST CANCER RES.
 PI Boel P, Boon-Falleur T, Coulie P, Szikora J, Van Der Bruggen P;
 PI Wildmann C;
 DR WPI; 95-292948/38.
 PT Identification of cells presenting HLA-C-clone 10 or MAGE-1 derived
 PT peptide - allows diagnosis and treatment of individuals with
 PT cellular abnormalities, e.g. melanoma, also HLA-Cw*1601 derived
 PT peptide(s)
 PS Claim 15; Page 19; 26pp; English.
 CC HLA-C-clone 10 is presented on the surface of certain abnormal cells,
 CC MAGE-1 is also expressed by these cells. R82215-R82217 and R89909 are
 CC peptides of such molecules that are expressed and presented on the
 CC surface of abnormal cells. The peptides are useful for the
 CC identification of abnormal cells and thus they allow diagnosis and
 CC treatment of cellular abnormalities, e.g. melanoma and other cancers.
 CC HLA-C-clone 10 is also known as HLA-Cw*1601.
 SQ Sequence 12 AA;

Query Match 3.4%; Score 141; DB 15; Length 12;
 Best Local Similarity 54.3%; Pred. No. 4.86e+00;
 Matches 19; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

Db e h s a y g e p r k l
 Dt 1 garcaywangcngcngcncmgnmnaarytnt 35
 Qy 4562 GAGCAGCTGCTATGGGAGCCCGAGGAGCTGCT 4596
 Qt E H S A Y G E P R K L

RESULT 9
 ID R80619 standard; Protein; 12 AA.
 AC R80619;
 DT 28-FEB-1996 (first entry)
 DE Immunogenic peptide of tumour rejection antigen (MAGE-1).
 DE Tumour rejection antigen; MAGE-1; monoclonal antibody; MAb;
 KW diagnosis; immunoassay; cancer; immunogen; antisera.
 OS Homo sapiens.
 PN W09520974-A1.
 PD 10-AUG-1995.
 PF 05-JAN-1995; U00095.
 PR 01-FEB-1994; US-190411.
 PA (LUDW-) LUDWIG INST CANCER RES.
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 PA (SLOK) MEMORIAL SLOAN-KETTERING CANCER CENT.
 PI Boon-falleur T, Chen Y, Garin-chesa P, Old LJ, Rettig WJ;
 PI Stockert E, Van der bruggen P;
 DR WPI; 95-283606/37.
 PT New monoclonal antibody binding specifically to MAGE-1 - useful for
 PT diagnosis and monitoring of cancer, also new hybridomas, recombinant
 PT MAGE-1 and immunogenic peptide(s)
 PS Claim 12; Page 20; 33pp; English.
 CC A monoclonal antibody directed against the tumour rejection antigen
 CC (MAGE-1) can be used to detect MAGE-1 in samples by standard
 CC immunoassay methods for diagnosis and monitoring of cancer etc. The
 CC monoclonal antibody is designated MA454 and is produced by the
 CC hybridoma deposited as ATCC HB11540. The monoclonal antibody is
 CC specific for MAGE-1, having no reactivity for MAGE-2 or MAGE-3.
 CC Peptide fragments of MAGE-1 (See R80618-20) may be useful as
 CC immunogens for production of the monoclonal antibody and antisera.
 SQ Sequence 12 AA;

Query Match 3.4%; Score 141; DB 15; Length 12;
 Best Local Similarity 61.1%; Pred. No. 4.86e+00;
 Matches 22; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Db l f r a v i t k k v a d
 Dt 1 yntntymgngcngtgnathacnaaraargtngcngay 36
 Qy 4169 TTGTCGAGCAGTATCACTAAGAGTGCTGAT 4204
 Qt L F R A V I T K K V A D

RESULT 10
 ID R40919 standard; Protein; 149 AA.
 AC R40919;
 DT 22-FEB-1994 (first entry)
 DE HPV E6 region product.
 KW Human papilloma virus; HPV; benign; malignant.

[illegible]

CC patients susceptible to MAGE associated tumours, e.g. melanomas.

SQ Sequence 10 AA;

Query Match 3.2%; Score 135; DB 13; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.19e+01;
Matches 18; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

Db d l v q e k y l e y
Dt 1 gayyngtncargaraartayyngartay 30
QV 4604 GATTTGGTGCAGGAAAGTACCTGGAGTAC 4633
Qt D L V Q E K Y L E Y

RESULT 12

ID R24393 standard; Protein; 351 AA.
AC R24393;
DT 22-NOV-1992 (first entry)
DE Sequence of Histidine-rich protein (HisRP).
KW Malaria vaccine; Histidine-rich protein; cytoadherence.
OS Plasmodium lophurae.
FH Key Location/Qualifiers
FT Modified site 40..42
FT /label= potential glycosylation site
FT Peptide 1..23
FT /label= signal 24..47
FT Peptide
FT /label= pro-peptide
PN US5116965-A.
PD 25-MAY-1992.
PF 26-AUG-1986; 900401.
PR 26-AUG-1986; US-900401.
PI (SLOK) SLOAN KETTERING INST CANCER.
PA Pologe L, Ravetch JV;
PI WPI; 92-199590/24.
DR N-PSDB; Q24393.
DT Histidine-rich protein associated with Plasmodium knob phenotype -
PT and DNA encoding it, used for in vitro diagnosis of P.
PT Falciparum infection.
PT Disclosure; Fig 7A-B; 29pp; English.
PS Two variants of HisRP are produced by P. falciparum. One is
CC associated with what is referred to as "knobby phenotype" (K30) and
CC "knobless phenotypes" (K-). The "knobby" and "knobless" phenotypes
CC have been implicated in cytoadherence, which is characteristic of
CC erythrocyte infection. It has now been found that cDNA expressing
CC both Kt and K- HisRP can be obtained by the use of P. lophurae HisRP
CC expressing DNA. The genomic clone (Q25532) is encoded in two
CC exons, separating the signal peptide-encoding sequence from the
CC pro-sequence, confirming that synthesis of the protein occurs via
CC the preproprotein. Oligo. probes synthesised to the signal
CC peptide-encoding exon reveal multiple homologous DNA sequences in
CC the P. lophurae genome. The sequence of mature proteins is arranged
CC in numerous tandem repeats with up to nine histidine residues in a
CC row, similar to other Plasmodium proteins for which sequence data
CC have so far been reported.
SQ Sequence 351 AA;

Query Match 3.2%; Score 135; DB 4; Length 351;
Best Local Similarity 36.4%; Pred. No. 1.19e+01;
Matches 43; Conservative 28; Mismatches 46; Indels 1; Gaps 1;

[illegible]

RESULT	15
ID	R47327 standard; Protein; 10 AA.
AC	R47327;
DE	31-AUG-1994 (first entry)
DT	HLA-A*3 MAGE 1 antigen peptide fragment 128-137.
KW	Immunogenic; HLA-A*3.2; HLA-A1; HLA-A11; binding motif; MHC molecule;
KW	immune response; viral infection; cancer; prostate cancer; lymphoma;
KW	hepatitis; AIDS; antibody; diagnosis; melanoma antigen.
OS	Synthetic.
PN	W09403205--A.

PD 17-FEB-1994.
 PF 06-AUG-1993; D07421.
 PR 07-AUG-1992; US-926666.
 PR 05-MAR-1993; US-027746.
 PA (CYTE-) CYTEL CORP.
 PI Celis E, Grey HM, Kubo RT, Sette A;
 DR WPI; 94-065403/08.
 PT Peptide which specifically binds selected MHC allele - used to
 PT induce an immune response for treatment or prevention of viral
 PT infection or cancer, or for diagnosis
 PS Example 8; Page 52; 150pp; English.
 CC The sequences given in R47304-33 and R49201-44 are immunogenic
 CC peptides which have a HLA-A3.2, HLA-A1 or a HLA-A11 binding motif.
 CC These peptides may be used in the composition of the invention.
 CC These peptides are capable of binding selected MHC molecules and
 CC inducing an immune response. They can be used to treat and/or
 CC prevent viral infection and cancer, eg. prostate cancer, lymphoma,
 CC hepatitis or AIDS. They can also be used to produce antibodies for
 CC use as diagnostic or therapeutic agents. The peptides can also be
 CC used as diagnostic agents.
 SQ Sequence 10 AA;

Query Match 3.1%; Score 127; DB 9; Length 10;
 Best Local Similarity 60.0%; Pred. No. 3.77e+01;
 Matches 18; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

Db m l e s v i k n y k
 Dt 1 atgtyngarwsgntnatharaayayaar 30
 QY 4262 ATGTCGAGAGTGTCACAAATTAACAAG 4291
 QT M L E S V I K N Y K

Search completed: Thu Apr 3 12:07:15 1997
 Job time : 98 secs.

 M P S R E L (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPSrch_ntp n.a. - n.a. Smith-Waterman search, using a protein database
 which has been backtranslated into n.a. using IUPAC symbols
 Run on: Thu Apr 3 12:09:54 1997; MasPar time 96.29 Seconds
 Tabular output not generated. 1332.228 Million cell updates/sec

Title: >US-08-190-411A-1

Description: (3931-4761) from 5541104.seq
 Perfect Score: 4155
 N.A. Sequence: 3931 GGCCCAACAAGAGCCCTGG.....CAAGAGTTCGCTTTTCTTC 4761
 Comp: CCGGGTTGTTCTCGGGACC.....GTTCTCAAGCGAAGAAAG

Scoring table: TABLE bktranslate2
 Gap 30

Nmatch STD : Dbase 0; Query 0

Searched: 82182 seqs, 77182545 bases x 2

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: pir48
 1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4
 8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unann
 14:unrev

Statistics: Mean 70.391; Variance 147.459; scale 0.477

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query	Length	ID	Description	Pred. No.
1	3009	72.4	JC2358	280	12	tumor-associated ant	0.00e+00
2	2361	56.8	JC2359	317	12	tumor-associated ant	0.00e+00
3	2103	50.7	JC2360	314	12	tumor-associated ant	0.00e+00
4	2103	50.6	JC2361	314	12	tumor-associated ant	0.00e+00
5	2064	49.7	JC2362	314	12	tumor-associated ant	0.00e+00
6	1030	24.8	S52167	347	11	MAGE-Xp protein - hu	1.31e-157
7	1030	24.8	I38008	347	11	MAGE-Xp protein - hu	1.31e-157
8	441	10.6	JN0148	325	12	necln, brain - mus	1.81e-47
9	149	3.6	W6WLHS	158	3	E6 protein - human p	4.13e-02
10	151	3.6	S42509	1041	11	Rag-1 protein - chic	2.43e-02
11	144	3.5	W6WL35	149	3	E6 protein - human p	1.52e-01
12	141	3.4	J01278	358	12	histamine H2 recepto	3.25e-01
13	143	3.4	S59701	970	10	PSU1 protein - yeast	1.96e-01
14	137	3.3	JC2359	317	12	tumor-associated ant	8.81e-01
15	137	3.3	S18649	342	11	homeotic protein HOX	8.81e-01
16	138	3.3	S00755	350	11	pleckstrin - human	6.88e-01
17	136	3.3	P00054	439	8	hypothetical protein	1.13e+00
18	137	3.3	S52418	846	12	Xlaas protein - rat	8.81e-01
19	133	3.2	A05192	74	9	hypothetical protein	2.32e+00
20	133	3.2	S44157	310	10	signal recognition p	2.32e+00
21	135	3.2	KGZQHL	351	3	histidine-rich glyco	1.44e+00
22	132	3.2	S27794	407	10	giant secretory prot	2.95e+00
23	131	3.2	A27117	491	4	cytochrome P450 2B5,	3.74e+00
24	131	3.2	S31278	491	4	cytochrome P450 2B4	3.74e+00
25	131	3.2	O4RBP	491	1	cytochrome P450 2B4	3.74e+00
26	131	3.2	S35666	491	4	cytochrome P450 2B4	3.74e+00
27	131	3.2	S31277	491	4	hypothetical protein	1.83e+00
28	134	3.2	S51409	648	9	hypothetical protein	3.74e+00
29	131	3.2	S25786	675	9	hypothetical protein	3.74e+00


```

RESULT      3
ENTRY       JC2360          #type complete
TITLE       tumor-associated antigen , MAGE-3b - human
ORGANISM    #formal name Homo sapiens #common name man
DATE        20-Feb-1995 #sequence revision 20-Feb-1995 #text_change
           15-Mar-1996

ACCESSIONS  JC2360
REFERENCE    Ding, M.; Beck, R.J.; Keller, C.J.; Fenton, R.G.
#authors     Biochem. Biophys. Res. Commun. (1994) 202:549-555
#journal      Cloning and analysis of MAGE-1-related genes.
#title        JC2360
#accession    ##molecule_type mRNA
              ##residues i-314 ##label DIN
              ##experimental_source melanoma cell line DMI50
GENETICS     MAGE-3b
FEATURE      168-176      #region HLA-A1 binding #status predicted
SUMMARY      #length 314 #molecular-weight 34891 #checksum 9870

Query Match      50.7%; Score 2105; DB 12; Length 314;
Best Local Similarity 47.4%; Pred. No. 0.00e+00;
Matches 369; Conservative 178; Mismatches 231; Indels 1; Gaps 1

Db   q e a a s s s s t l v e v t l g e v p a
Dt   rcargcngcnswanwsnwnacnhtngtngargtnacnytgnggargtncngc 164
QY   GCAGGGTGCCACTCTCTCTCTCTCTCTGTCGTCTGCGACCCTGCAGGAGTGCCCAC 4023
Qt   Q A A T S S S S P L V L G T L E E V P T

Db   a e s p d p p q s p q g a s s l p t t m
Dt   ngcngarwncngayccncncrcarwscncncargngcgnwswnytcnnaacnat 224
QY   TGCTGGTCAACAGATCCTCCCAGAGTCTCAGGAGCCTCCGCCTTTCCCATACCAT 4083
Qt   A G S T D P P Q S P Q G A S A F P T I

Db   n y p l w s q s y e d s s n q e e e g p
Dt   gaaytaycnyntgtgwancrwnstaygayyswnswnaaycargargagrgncc 284
QY   CAACITTCATCCAGAGGCAACCCAGTAGGGGTTTCAGCAGCCGTCGAAGGAGGGGCC 4143
Qt   N F T R Q R Q P S E G S S S R E E E G P

Db   s t f p d l e s e f q a a l s r k v a k
Dt   nwsnacntyccngyngarwsgarttycargcngcnytwsmngnarngtungchna 344
QY   AAGCACCCTTGTATCTCGGAGTCTTGTCCGAGCAGTAGTAATCACTAAGAAGTGCGTGA 4203
Qt   S T S C I L E S L F R A V I T K K V A D

Db   l v h f l l k y r a r e p v t k a e m
Dt   rytngtncayttynytntyaartaaymgcmgmgarccngtngnchnaarcngdarat 404
QY   TTGTGGTGTGTTTCTGCTCTCAAATAATFCAGCAGGAGGCGCATCAAAAGCAGCAAT 4263
Qt   L V G F L L L K Y R A R E P V T K A E M

Db   l g s v v g n w q y f f p v i f s k a s
Dt   gytyngdnwgntngtngngaaytgcgcarttyttyccngtngnthctywsnarcnw 464
QY   GTTGAGAGTGTCATCAAAAATATACAGCAATCTGTTTCTTGAGATTCTGCGAAGCCTC 4323
Qt   L E S V I K N Y K H C F P E I F G K A S

```

[illegible]

GENETICS

[illegible][illegible]

[illegible]

Dd	q q n y l k y q i v p h i e p p e y e f
Dt	731 tncarcaraaycayynaaartaycaymngntcncayathgarccnccngartaygart 790
Qy	6611 TGcAGGAAAGTACCTGGAGTACG--GCAAGTTCGCGGACAGTGATCCGCGACGCTATGAT 4669
Qt	Q E K Y L E Y X Q V P D S D P A R Y E F
Dd	f w g s r a n r e i t k m q i m e f l a
Dt	791 tyctygggnwnmgncnaaymgngarathacnaaratgcarrathatgagartyying 850
Qy	4670 TCCTGTGGGTCCAAAGGCCCTCGCTGAACACAGCTATGTCAAAAGTCTTGAGTATGTA 4729
Qt	L W G P R A L A E T S Y V K V L E Y V I
Dd	r v f k k d
Dt	851 cmmgnginttyaaraadayc 871
Qy	4730 TCAAGTCTAGTGCAGAGTTC 4750
Qt	K V S A R V
RESULT	9
ENTRY	W6WLHS #type complete
TITLE	E6 protein - human papillomavirus type 16
ORGANISM	#formal_name human papillomavirus type 16
DATE	28-May-1986 #sequence_revision 28-May-1986 #text_change 02-May-1994
ACCESSION	A03682
REFERENCE	A22355
#authors	Seedorff, K.; Krammer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.
#journal	Virology (1985) 145:181-185
#title	Human papillomavirus type 16 DNA sequence.
#cross-references	MDID:85246220
#accession	A03682
#molecule_type	DNA
#residues	1-158 #label SEE
CLASSIFICATION	#superfamily papillomavirus E6 protein
KEYWORDS	early protein; zinc finger
SUMMARY	#length 158 #molecular-weight 19187 #checksum 9827
Query Match	3.6%; Score 149; DB 3; Length 158;
Best Local Similarity	34.3%; Pred. No. 4.13e-02;
Matches	37; Conservative 29; Mismatches 41; Indels 1; Gaps 1
Dd	c l k f y s k i s e y i r h y c y s l y g
Dt	215 artggyynaaartcaywnaaarathwngartaymgncaycaytgytaywsnyntayg 274
Cp	4295 AGTGCCTGTAATTTTGTATGACACCTCC-AGCAATTTCGCTTTGACTGCGCTCCTG 4237
Ct	C L * F L M T L S x H F C L C D W L P G
Dd	t t l e q q y n k p l c d l l
Dt	275 gnaacnctyngarcartayaaarccnctyngayvyntyna 322
Cp	4236 GCTCGATATTGAGGACGAACCAACCAATCAGCCACCTTCTTA 4189
Ct	S I F E E Q K T N Q I S H L L
RESULT	10
ENTRY	S42509 #type complete
TITLE	Rag-1 protein - chicken

ORGANISM	#formal name Gallus gallus #common name chicken
DATE	07-Sep-1994 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995
ACCSSION	S42509
REFERENCE	S42509
authors	Carlson, L.M.; Oettinger, M.A.; Schatz, D.G.; Masteller, E.L.; Hurley, E.A.; McCormack, W.T.; Baltimore, D.; Thompson, C.B.
#journal	Cell (1991) 64:201-208
#title	Selective expression of RAG-2 in chicken B cells undergoing immunoglobulin gene conversion.
#accession	S42509
##status	preliminary
##molecule_type	DNA
##residues	1-1041 ##label CAR
##cross-references	GB:M58530
##note	the nucleotide sequence was submitted to the EMBL Data Library, February 1991
##note	neither the amino acid nor nucleotide sequence is given in this paper
SUMMARY	#length 1041 #molecular-weight 119916 #checksum 3766
Query Match	3.6%; Score 151; DB 11; Length 1041;
Best Local Similarity	45.3%; Pred. No. 2.43e-02;
Matches	39; Conservative 14; Mismatches 33; Indels 0; Gaps 0;
Db	k d e e v p r g e k l i l t q k d f m g
Dt	185 ayaargavgargtgtncnmngngaraarytnathynacnaraargaytyatgg 244
Cp	4473 ACAATTATCAGGAAGCCTGCTTGGGCATGCTGATTATCATCCAGCAGGCCATCATAG 4414
Ct	N Y Q E A C L G H D L I I T Q Q A I I G
Db	n t q a l e k d
Dt	245 gnaayacncargcnyntngaraargay 270
Cp	4413 GAGAGACCTAGGAGGTGACAAGGAC 4388
Ct	E T * A G D K D
RESULT 11	
ENTRY	W6WL35 #type complete
TITLE	E6 protein - human papillomavirus type 35
ORGANISM	#formal name human papillomavirus type 35
#note	host Homo sapiens (man)
DATE	30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 05-Jan-1996
ACCSSION	E40824; S36521
REFERENCE	A40824
authors	Marich, J.E.; Pontsler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.
#journal	Virology (1992) 186:770-776
#title	The phylogenetic relationship and complete nucleotide sequence of human papillomavirus type 35.
#cross-references	MUID:92124753
#accession	E40824
##molecule_type	DNA
##residues	1-149 ##label MAR
##cross-references	GB:M74117
##note	translation of the nucleotide sequence is not given
REFERENCE	S36469

#authors Delius, H.; Hofmann, B.
#submission submitted to the EMBL Data Library, August 1993
#accession S36521
#status preliminary
#molecule_type DNA
#residues 1-149 **#label** DEL
#cross-references EMBL:X74477
#experimental_source strain 35H
CLASSIFICATION superfamily papillomavirus E6 protein
KEYWORDS early protein; zinc finger
SUMMARY **#length** 149 **#molecular-weight** 18045 **#checksum** 914

Query Match 3.5%; **Score** 144; **DB** 3; **Length** 149;
Best Local Similarity 33.2%; **Pred.** No. 1.52e-01;
Matches 38; **Conservative** 28; **Mismatches** 41; **Indels** 1; **Gaps** 1;

Db	c	l	k	f	y	s	k	i	s	e	y	r	w	y	r	y	s	v	y	q	
Dt	194	artgytnaar	tyav	wn	aa	rthw	ng	artay	mg	nt	ggtay	mg	ntay	ws	ng	tntay	g	253			
		l:l:l:l:l	l:l:l:l:l	l:l:l:l:l	l:l:l:l:l	l:l:l:l:l	l:l:l:l:l	l:l:l:l:l	l:l:l:l:l	l:l:l:l:l	l:l:l:l:l	l:l:l:l:l	l:l:l:l:l	l:l:l:l:l	l:l:l:l:l	l:l:l:l:l	l:l:l:l:l				
Cp	4295	ACTGCTGTTAA	TTTGATG	AGCA	CTCC	-AC	ATTC	TGCG	CTTG	CACTG	CGCTCC	CG	4237								
Ct		C	L	*	F	L	M	T	L	S	S	H	F	C	L	C	D	W	L	P	G
Db	e	t	l	e	a	k	q	c	n	k	q	l	c	h	l						
Dt	254	ngaracnytn	gark	cat	g	aa	ya	ar	ca	ry	tntg	cy	ay	tn	th	na	301				
		l:l:l:l:l	l:l:l:l:l	l:l:l:l:l	l:l:l:l:l	l:l:l:l:l	l:l:l:l:l	l:l:l:l:l	l:l:l:l:l	l:l:l:l:l	l:l:l:l:l	l:l:l:l:l	l:l:l:l:l	l:l:l:l:l	l:l:l:l:l	l:l:l:l:l					
Cp	4236	GCTCGATAT	TTCAG	AGC	AGAA	CCACC	AAAT	CAG	CGAC	CTTCT	TA	4189									
Ct		S	I	F	E	E	Q	K	T	N	Q	I	S	H	L	L					

RESULT 12
ENTRY JQ1278 **#type** complete
TITLE histamine H2 receptor - rat
ORGANISM **#formal_name** *Rattus norvegicus* **#common_name** Norway rat
DATE 31-Mar-1992 **#sequence_revision** 31-Mar-1992 **#text_change** 09-Sep-1994
ACCESSIONS JQ1278
REFERENCE JQ1278
#authors Ruat, M.; Traiffort, E.; Arrang, J.M.; Leurs, R.; Schwartz, J.C.
#journal Biochem. Biophys. Res. Commun. (1991) 179:1470-1478
#title Cloning and tissue expression of a rat histamine H2-receptor gene.
#cross-references MIMD:92028890
#accession JQ1278
#molecule_type DNA
#residues 1-358 **#label** R0A
KEYWORDS G protein-coupled receptor; glycoprotein; transmembrane protein

FEATURE
 22-45 **#domain** transmembrane **#label** TM1\
 58-81 **#domain** transmembrane **#label** TM2\
 93-113 **#domain** transmembrane **#label** TM3\
 136-159 **#domain** transmembrane **#label** TM4\
 178-203 **#domain** transmembrane **#label** TM5\
 234-260 **#domain** transmembrane **#label** TM6\
 267-288 **#domain** transmembrane **#label** TM7\
 4 **#binding_site** carbohydrate (Asn) (covalent) **#status** predicted\
 220,311,315 **#binding_site** phosphate (Ser) (covalent) **#status** predicted

```
SUMMARY      #length 358 #molecular-weight 40253 #checksum 3245

Query Match      3.4%; Score 141; DB 12; Length 358;
Best Local Similarity 30.3%; Pred. No. 3.25e-01;
Matches 40; Conservative 36; Mismatches 54; Indels 2; Gaps 1;

Db      h c k f a s h n s h k t s l r l n n s l
Dt      905 tycaygyarttygnwnscayawncayaaaracwnsytmngnytnaayaweny 964
Cp      4494 TCATTGCAATCATACCAAGGACAATATACGAAAGCCGTCTTGGGCATGAT--CTGAT 4437
Ct      H C N H D Q D N Y Q E A C L G H D x * L

Db      l p r s q s r e g r w q e e k p l k l q
Dt      965 thntcnmgnwancarmngngtgargumngtgargargaraarccnytnaarytnc 1024
Cp      4436 TATCACCACGAGCCATCATAGGAGAGACCTAGGACAGCTAGGACATAGGAGTGCC 4377
Ct      S P S R P S * E R P R Q V T R T * E W P

Db      v w s
Dt      1025 argntggwang 1036
Cp      4376 CGGTGGGTCTG 4365
Ct      V G S

RESULT 13
ENTRY   S59701 #type complete
TITLE   PS01 protein - yeast (Saccharomyces cerevisiae)
ORGANISM #formal name Saccharomyces cerevisiae
DATE     13-Jan-1996 #sequence_revision 16-Feb-1996 #text_change
        16-Feb-1996
ACCESSIONS S59701
REFERENCE   Tzagoloff, A.A.
#authors   Submitted to the EMBL Data Library, June 1995
#description Suppressor of a yeast pet mutant.
#accession S59701
#molecule_type DNA
#residues 1-970 #label TZA
#cross-references EMBL:L43065
#experimental_source strain D273-10B
GENETICS
#gene      PS01
SUMMARY    #length 970 #molecular-weight 108682 #checksum 2450

Query Match      3.4%; Score 143; DB 10; Length 970;
Best Local Similarity 42.3%; Pred. No. 1.96e-01;
Matches 30; Conservative 19; Mismatches 20; Indels 1; Gaps 1;

Db      s k l i s q d i l k e n n f q d g e v p
Dt      1953 ywnaarytnathwncargavathytnaargaaaytytcargaygngargntcc 2012
Cp      4585 CAGACAGCTCTCACCACAGATTGTGTCAGGAAATCTACCTGGAGTACGCG-AGGTGCC 4643
Ct      R K L L T Q D L V Q E K Y L E Y G x v p

Db      h r d
Dt      2013 ncaymngay 2022
Cp      4644 GGACAGTGAT 4653
Ct      D S D
```

```
RESULT 14
ENTRY   JC2359 #type complete
TITLE   tumor-associated antigen , MAGE-X2 - human
ORGANISM #formal name Homo sapiens #common name man
DATE     20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
        15-Mar-1996
ACCESSIONS JC2359
REFERENCE   JC2358
#authors   Ding, M.; Beck, R.J.; Keller, C.J.; Fenton, R.G.
#journal   Biochem. Biophys. Res. Commun. (1994) 202:549-555
#title     Cloning and analysis of MAGE-1-related genes.
#accession JC2359
#molecule_type mRNA
#residues 1-317 #label DIN
#experimental_source melanoma cell line DM150
GENETICS
#gene      MAGE-X2
FEATURE    #region HLA-A1 binding #status predicted
169-177    #length 317 #molecular-weight 34928 #checksum 9004
SUMMARY    #length 317 #molecular-weight 34928 #checksum 9004

Query Match      3.3%; Score 137; DB 12; Length 317;
Best Local Similarity 31.9%; Pred. No. 8.81e-01;
Matches 30; Conservative 27; Mismatches 36; Indels 1; Gaps 1;

Db      n e g s s q e e g p s t s p d a e s
Dt      253 aaygargnwnwnswncargargarggnccnwnsnacnwgngayngarwsn 312
Cp      4173 AACAGGACTCCAGATACAGAGGTGCTTGCCCTCTTCCAC-GGCTGCTGAACC 4115
Ct      N K D S R I Q E V L G P S S S X A A G T

Db      l f r e a l s n k v d
Dt      313 yntttmngngargcnytnwnsnaayaargtngayg 346
Cp      4114 CTCCTGGTGGCTCTGTCGAGTGAAGTTGATG 4081
Ct      L T G L P L S S E V D

RESULT 15
ENTRY   S18649 #type complete
TITLE   homeotic protein HOX D9 - human
ALTERNATE_NAMES homeotic protein Hox 4c; homeotic protein Hox 5.2
ORGANISM #formal name Homo sapiens #common name man
DATE     13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
        01-Mar-1996
ACCESSIONS S18649; S05958; S14935; A32830
REFERENCE   S18649
#authors   Zappavigna, V.; Renucci, A.; Izpisua-Belmonte, J.C.; Urier,
#journal   G.; Peschle, C.; Duboule, D.
#title     EMBO J. (1991) 10:4177-4187
#accession S18649
#molecule_type mRNA
#residues 1-342 #label ZAP
#cross-references EMBL:X59372
#note      intron position was determined by sequencing of genomic
        and cross-regulatory capacities.
```

REFERENCE	DNA
#authors	A32830
#journal	Oliver, G.; Sidell, N.; Fiske, W.; Heinzmann, C.; Mohandas, T.; Sparkes, R.S.; De Robertis, E.M.
#title	Genes Dev. (1989) 3:641-650
#cross-references	Complementary homeo protein gradients in developing limb buds.
#accession	#cross-references MUID:89306602
#molecule_type	S03958
#residues	264-265
#cross-references	EMBL:X15506

#cross-references EMBL:X13066
S07541

REFERENCE
#authors Acampora, D.; d'Esposito, M.; Faiella, A.; Fannese, M.;
Migliaccio, E.; Morelli, F.; Stornaiuolo, A.; Nigro, V.;
Simeone, A.; Boncinelli, E.
#journal Nucleic Acids Res. (1989) 17:10385-10402
#title The human HOX gene family.
#cross-references MIMD:90098876
#accession S14935
#molecule type DNA
#residues_ 275-340 #label ACA

GENETICS

#gene GDB:HOXD9

#cross-references GDB:G00-120-678

#map_position 2q31

#introns 263/1

CLASSIFICATION #superfamily homeobox homology

KEYWORDS DNA_binding; homeobox

FEATURE

276-332

SUMMARY

#domain homeobox homology #label HOX

#length 342 #molecular-weight 35580 #checksum 1965

Query Match 3.3%; Score 137; DB 11; Length 342;
Best Local Similarity 20.2%; Pred. No. 8.81e-01;
Matches 19; Conservative 35; Mismatches 40; Indels 0; Gaps 0;

Db s s s t g l s s s k r t e c g s v a r e
Dt w s n w s n y n u n w s n w s n a a r m g n a c g t g y w a n g t n g m m g n g a r 564
:: :: | | : : : : : : : : | : : : | : :
4521 t c t g g a g a c t g a t g t c a g g t c t a t g g g a g c a c g a c t g c c t a t g g g 4580
QY s g r s * w R G C T M M G G S T V P M G

Db	s q g s s g p e f s c
Dt	565 wencargnwnngncgcagattwywtgta 598 : : : : : : : : : 4581 ACCCAGGAGTGTCACCCAAATTTGGTCCA 4614 S P G S C S S P K I W C
Qy	
Or	

Search completed: Thu Apr 3 12:12:58 1997
Job time : 184 secs.

[illegible]

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MPsrch ntp n.a. - n.a. Smith-Waterman search, using a protein database which has been backtranslated into n.a. using IUPAC symbols

Run on: Thu Apr 3 12:07:32 1997; MasPar time 68.30 Seconds
1352.803 Million cell updates/sec
Tabular output not generated.

```

Title: >US-08-190-411A-1
Description: (931-4761) from 5541104.seq
Perfect Score: 4155
N.A. Sequence: 3931 GCGCCACACAGAGGCCCTGG.
Comp: CCGGTTGTTCTCCGGGACC.

```

Scoring table: TABLE bktranslate2
Gap 30

Nmatch STD : Dbase 0; Query 0
Searched: 52205 seqs, 55594155 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot.33

Database:
swiss-prot33
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10

Statistics: Mean 72.427; Variance 118.755; scale 0.610

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query				Description	Pred. No.
	Score	Match	Length	ID		
1	3176	76.4	309	MAG1_HUMAN	MELANOMA-ASSOCIATED A	0.00e+00
2	2361	56.8	317	MAG6_HUMAN	MELANOMA-ASSOCIATED A	0.00e+00
3	2105	50.7	314	MAG3_HUMAN	MELANOMA-ASSOCIATED A	0.00e+00
4	2103	50.6	314	MAG3_HUMAN	MELANOMA-ASSOCIATED A	0.00e+00
5	2035	49.5	314	MAG2_HUMAN	MELANOMA-ASSOCIATED A	0.00e+00
6	2049	49.3	314	MAG2_HUMAN	MELANOMA-ASSOCIATED A	0.00e+00
7	1671	40.2	315	MAG9_HUMAN	MELANOMA-ASSOCIATED A	0.00e+00
8	1533	36.9	319	MAGY_HUMAN	MELANOMA-ASSOCIATED A	0.00e+00
9	1525	36.7	369	MAGX_HUMAN	MELANOMA-ASSOCIATED A	0.00e+00
10	1278	30.8	234	MAG8_HUMAN	MELANOMA-ASSOCIATED A	1.99e-262
11	1030	24.8	347	MAGA_HUMAN	MELANOMA-ASSOCIATED A	8.89e-201
12	632	15.2	124	MAGP_HUMAN	MELANOMA-ASSOCIATED A	1.69e-104
13	441	10.6	325	NPCD_MOUSE	MELANOMA-ASSOCIATED A NPCDN.	1.24e-60

Search completed: Thu Apr 3 12:12:58 1997
Job time : 184 secs.

[illegible]

DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE MELANOMA-ASSOCIATED ANTIGEN 4 (MAGE-4 ANTIGEN) (MAGE-X2).
GN MAGE4.
GS HOMO SAPIENS (HUMAN).
GC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=BLOOD;
RC MEDLINE; 95012457.
RX DE PLAEN E., ARDEN K., TRAVERSARI C., GAFORIO J.J., SZIKORA J.-P.,
RA DE SMET C., BRASSEUR F., VAN DER BRUGGEN P., LETHE B., LURQUIN C.,
RA BRASSEUR R., CHOMEZ P., DE BACKER O., CAVENEE W., BOON T.;
RL IMMUNOGENETICS 40:360-369(1994).
RN [2]
RN SEQUENCE FROM N.A.
RC TISSUE=SKIN;
RC MEDLINE; 94311935.
RX DING M., BECK R.J., KELLER C.J., FENTON R.G.;
RL BIOCHEM. BIOPHYS. RES. COMMUN. 202:549-555(1994).
CC -!- FUNCTION: NOT KNOWN, THOUGH MAY PLAY A ROLE IN EMBRYONAL
CC DEVELOPMENT AND TUMOR TRANSFORMATION OR ASPECTS OF TUMOR
CC PROGRESSION.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES,
CC SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LONG
CC CARCINOMA AND BREAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT
CC FOR TESTES AND PLACENTA.
CC -!- SIMILARITY: BELONGS TO THE MAGE FAMILY. STRONG SIMILARITY WITH
CC MAGE-1.
CC EMBL; U10687; G533515; -.
CC EMBL; U10688; G533517; -.
CC EMBL; U10340; G499124; -.
CC ANTIGEN; MULTIGENE FAMILY; POLYMORPHISM; TUMOR ANTIGEN.
CC DOMAIN; 41 44 POLY-SER.
CC VARIANT 173 173 T -> A.
CC CONFLICT 307 307 E -> Q (IN REF. 2).
CC SEQUENCE 317 AA; 34929 MW; 3CE38AF9 CRC32;
CC SQ
Query Match 56.8%; Score 2361; DB 5; Length 317;
Best Local Similarity 49.9%; Pred.No. 0.00e+00;
Matches 395; Conservative 174; Mismatches 221; Indels 1; Gaps 1;

Dbb	a	a	v	s	s	s	s	p	l	v	p	g	t	l	e	e	v	d	a	a
Dt	110	argcngcgt	nawswncn	ctngtcncngcnacny	tgardgavrgcncgcng	169														
		::	:::	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:
Qy	3966	AGSGCTGCAC	CGTCCTCCTCTGCTGTGCTGGCA	CCCTGGAGAGTGGCCACTG	4025															
Qt	A	A	T	S	S	P	L	G	T	L	E	E	V	P	T	A				
Dbb	e	s	a	g	s	p	q	s	p	q	g	a	l	p	t	i	s			
Dt	170	cngarwsgcngmcncnc	carwsncncargcgcnwsgcnytcncnacnathw	229																
		::	:::	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	
Qy	4026	CTCGGTCAACA	GATCTCTCCCACGATGCTTGAGGACGCTCCGCCCTTCCCCACTACCACCA	4085																
Qt	G	S	T	D	P	P	Q	S	P	Q	G	A	S	A	F	P	T	I	N	
Dbb	f	t	c	w	r	q	p	n	e	g	s	s	q	e	e	e	p	s		
Dt	230	snftyactntgytgmgn	cdarcnaaygarvgcwnswncn	cargargargcngcnw	289															
		::	:::	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	
Qy	4086	ACTCTTCGAC	GCAGCACCCAGTAGTGAGGGTTTCAGAGCCGTCRTEAAGAGGGGGCCAA	4145																
Qt	F	T	R	Q	R	Q	P	S	E	G	S	C	G	E	E	E	G	P	S	

Db 731 tncarcaraaytavylnaartaycamngtncncncayathqarccnccngartaygart 790
 Qy 4611 TGAGGAAAGTACCTGGAGTAGG-GCAGTGCAGGAGAGTATCCCGCAGCGCTATGAGT 4669
 Qc Q E K Y L E Y X Q V P D S D P A R Y E F
 Db f w g s r a n r e i t k m q i m e f l a
 Dt 791 tytttgggggnwmgngnaaymgngarathacnaaratgcathatgagrttytng 850
 Qy 4670 TCGTGGGTGCAAGGCGCTCGTGAACCCAGCTATGTAAGTCTTGAATATGA 4729
 Qc L W G P R A L A E T S Y V K V L E Y V I

Db 851 cmngntnttyaaraargayc 871
 Dt 4730 TCAAGGTCACTGCAAGAGTTC 4750
 Qc K V S A R V

RESULT 14
 ID V26 HPV16 STANDARD; PRT; 158 AA.
 AC P03126;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
 DE E6 PROTEIN.
 GN E6.

OS HUMAN PAPILLOMAVIRUS TYPE 16.
 OC VIRIDAE; DS-DNA NONENVELOPED VIRUSES; PAPAPOVIRIDAE; PAPILLOMAVIRUSES.
 [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE; 85246220.
 RA SEDORF K., KRAMMER G., DURST M., SUHAI S., ROWEKAMP W.G.;
 RL VIROLOGY 145:181-185(1985).
 [2]

RN SEQUENCE OF 31-50 FROM N.A.
 RP MEDLINE; 90218027.
 RX SCHNEIDER-MAUNOURY S., PEHAU-ARNAUDET G., BREITBURD F., ORTH G.;
 RL J. GEN. VIROL. 71:809-817(1990).
 CC -!- FUNCTION: THIS PROTEIN HAS TRANSFORMING ACTIVITY IN VITRO.
 CC -!- FUNCTION: EXHIBIT A STRONG, BUT NON SPECIFIC AFFINITY FOR DOUBLE
 CC STRANDED DNA (IN VITRO).
 CC -!- SUBCELLULAR LOCATION: NUCLEAR MATRIX-ASSOCIATED.
 CC -!- HPV16, IN COMPARISON TO HPV TYPES 6 AND 11, IS MORE OFTEN
 CC ASSOCIATED WITH MALIGNANT GENITAL CANCERS IN HUMANS.

DR EMBL; K02718; G333032; -.
 DR EMBL; D00735; G222373; -.
 DR PIR; A03682; W6WLHS.
 KW EARLY PROTEIN; DNA-BINDING; NUCLEAR PROTEIN; ZINC-FINGER;
 KW TRANSFORMING PROTEIN.
 FT ZN_FING 37 73 POTENTIAL.
 FT ZN_FING 110 146 POTENTIAL.
 SQ SEQUENCE 158 AA; 19187 MW; 3C576FA0 CRC32;

Query Match 3.6%; Score 149; DB 9; Length 158;
 Best Local Similarity 34.3%; Pred. No. 1.94e-03;
 Matches 37; Conservative 29; Mismatches 41; Indels 1; Gaps 1;

Db 215 artgyttnaarttyawnaarathwngartaymncaytaytgytawnyntayg 274
 Dt C l k f y s k i s e y r h y c y s l y g

Cp 4295 AGTGTGTAATTTTGTGACACTCC-AGCAATTCCTGCTTGTGAGTGCCTCG 4237
 Ct C L * F L M T L S x H F C L C D W L P G
 Db t t l e q q y n k p l c d l l
 Dt 275 gnacnacngarcacartayaayacnnyntngygvnytna 322
 Ct 4236 GCTGATATTGAGGAGCAGAAACCAACCAATFACGCCACTTCTTA 4189
 Ct S I F E E Q K T N Q I S H L L

RESULT 15
 ID RAG1 CHICK STANDARD; PRT; 1041 AA.
 AC P24271;
 DT 01-MAR-1992 (REL. 21, CREATED)
 DT 01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
 DT 01-MAR-1992 (REL. 21, LAST ANNOTATION UPDATE)
 DE V(D)J RECOMBINATION ACTIVATING PROTEIN.
 GN RAG-1.

OS GALUS GALLUS (CHICKEN).
 OC EURARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;
 OC GALLIFORMES.
 [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE; 91098648.
 RA CARLSON L.M., OETTINGER M.A., SCHATZ D.G., MASTELLER E.L.,
 RA HURLEY E.A., MCCORMACK W.I., BALTIMORE D., THOMPSON C.B.;
 RL CELL 64:201-208(1991).

CC -!- FUNCTION: RAG1 & RAG2 SYNERGISTICALLY ACTIVATE THE IMMUNOGLOBULIN
 CC V-D-J RECOMBINATION. V-D-J RECOMBINATION IS THE COMBINATORIAL
 CC PROCESS BY WHICH DEVELOPING LYMPHOCYTES BEGIN TO GENERATE THEIR
 CC ENORMOUS RANGE OF BINDING SPECIFICITIES FROM A LIMITED AMOUNT OF
 CC GENETIC INFORMATION.
 CC -!- SUBCELLULAR LOCATION: NUCLEAR.
 CC -!- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.

DR EMBL; M58530; G212623; -.
 DR PIR; S42509; S42509.
 DR PROSITE; PS00518; ZINC FINGER C3HC4.
 KW ZINC-FINGER; DNA-BINDING; NUCLEAR PROTEIN.
 FT ZN_FING 284 327 C3HC4-TYPE.
 SQ SEQUENCE 1041 AA; 119916 MW; 5858952 CRC32;

Query Match 3.6%; Score 151; DB 7; Length 1041;
 Best Local Similarity 45.3%; Pred. No. 1.01e-03;
 Matches 39; Conservative 14; Mismatches 33; Indels 0; Gaps 0;

Db k d e e v p r g e k l i l t q k d f m g
 Dt 185 ayaargaygargtncnmgngngaraarytnathynacnaargayttagg 244
 Ct 4473 ACAATTATCAGGAGCCTGTCTTGGCATGATCATATATCACCAGCAGCCATCATAG 4414
 Ct N Y Q E A C L G H D L I I T Q Q A I I G

Db n t q a l e k d
 Dt 245 gnaayacnargcnyntngaraargay 270
 Ct 4413 GAGAGCCTAGGAGGTGACAGGAC 4388
 Ct E T * A G D K D

Search completed: Thu Apr 3 12:09:37 1997

(2-2)

Job time : 125 secs.

MAPIREH (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Apr 3 11:57:27 1997; MasPar time 1.78 Seconds
81.020 Million cell updates/sec

Tabular output not generated.

Title: >US-08-190-411A-2
Description: (1-14) from 5541104.pep
Perfect Score: 93
Sequence: 1 INFTRQRPSEGSS 14

Scoring table: PAM 150
Gap 15

Searched: 88003 seqs, 10295656 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq25
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18

Statistics: Mean 17.740; Variance 50.911; scale 0.348

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	93	100.0	14 15	R80618	Immunogenic peptide o	3.60e-04
2	93	100.0	309 13	R70909	Human melanoma antige	3.60e-04
3	57	61.3	909 10	R50092	Humanised anti-CEA af	8.95e+00
4	55	59.1	96 1	P81863	Sequence encoded by L	1.51e+01
5	53	57.0	9 13	R65121	MAGE 1 immunogenic pe	2.53e+01
6	53	57.0	96 3	R12258	HIV-1 strain OYI open	2.53e+01
7	53	57.0	342 17	R95054	TGF-a-DETA-DGALA4 mult	2.53e+01

Caputa

560024

8	53	57.0	414	7	R36807	Pseudomonas exotoxin	2.53e+01
9	53	57.0	414	7	R32455	PE amino acids 2-414.	2.53e+01
10	53	57.0	419	2	R07054	PE40AB protein compri	2.53e+01
11	53	57.0	420	2	R06447	TGF-57-Pseudomonas ex	2.53e+01
12	53	57.0	420	2	R06993	PE40AB protein compri	2.53e+01
13	53	57.0	420	4	R20200	TGF-alpha-PE40AB.	2.53e+01
14	53	57.0	420	2	R06449	TGF-alpha-PE40-Ab mod	2.53e+01
15	53	57.0	421	17	R95055	IL-2-DETA-DGALA4 mult	2.53e+01
16	53	57.0	426	7	R32454	PE(2-414)-Ma(57-68) h	2.53e+01
17	53	57.0	426	17	R31735	Heregulin-PE40 HAR-TX	2.53e+01
18	53	57.0	496	1	R04934	Immunotoxin hybrid of	2.53e+01
19	53	57.0	530	17	R95053	scFv(FRP5)-DETA-DGALA	2.53e+01
20	53	57.0	557	1	R04923	Immunoprotein TANG11.	2.53e+01
21	53	57.0	574	1	R04919	Immunoprotein PEX45.	2.53e+01
22	53	57.0	577	1	R04924	Immunoprotein TANG12.	2.53e+01
23	53	57.0	613	8	R40112	Pseudomonas exotoxin	2.53e+01
24	53	57.0	613	8	R40106	Pseudomonas exotoxin	2.53e+01
25	53	57.0	613	8	R40110	Pseudomonas exotoxin	2.53e+01
26	53	57.0	613	8	R40102	Pseudomonas exotoxin	2.53e+01
27	53	57.0	613	8	R40105	Pseudomonas exotoxin	2.53e+01
28	53	57.0	613	8	R40113	Pseudomonas exotoxin	2.53e+01
29	53	57.0	613	8	R40109	Pseudomonas exotoxin	2.53e+01
30	53	57.0	613	8	R40111	Pseudomonas exotoxin	2.53e+01
31	53	57.0	613	8	R40104	Pseudomonas exotoxin	2.53e+01
32	53	57.0	614	16	R87738	Native pseudomonas ex	2.53e+01
33	53	57.0	637	5	R26982	(FRP5)-ETA fusion pro	2.53e+01
34	53	57.0	637	5	R26983	(FRP51)-ETA fusion pr	2.53e+01
35	53	57.0	632	7	R32456	PE with inactivated t	2.53e+01
36	53	57.0	652	7	R36808	Pseudomonas Exotoxin	2.53e+01
37	53	57.0	665	7	R32453	PE(2-414)-M1(2-252) h	2.53e+01
38	53	57.0	667	8	R39573	Sequence of 741 sfv-p	2.53e+01
39	53	57.0	668	7	R32457	PE having M1 residues	2.53e+01
40	53	57.0	670	7	R32468	BSPEMIC5aa fragment.	2.53e+01
41	53	57.0	670	7	R36820	PE-Influenza A virus	2.53e+01
42	53	57.0	746	7	R32458	PE having M1 residues	2.53e+01
43	53	57.0	746	7	R36810	Full-length PE with I	2.53e+01
44	53	57.0	917	7	R36821	PE binding/translocat	2.53e+01
45	53	57.0	937	7	R32470	PE binding and transl	2.53e+01

ALIGNMENTS

RESULT 1
ID R80618 standard; Protein; 14 AA.
AC R80618;
DE 28-FEB-1996 (first entry)
DE Immunogenic peptide of tumour rejection antigen (MAGE-1).
KW Tumour rejection antigen; MAGE-1; monoclonal antibody; MAb;
KW diagnosis; immunoassay; cancer; immunogen; antisera.
OS Homo sapiens.
PN WO9520974-A1.
PD 10-AUG-1995.
PF 05-JAN-1995; U00095.
PR 01-FEB-1994; US-190411.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
PI Boon-fallour T, Chen Y, Garin-chesa P, Old LJ, Rettig WJ;
PI Stockert E, Van der bruggen P;
DR WPI; 95-283606/37.

PT New monoclonal antibody binding specifically to MAGE-1 - useful for
 PT diagnosis and monitoring of cancer, also new hybridomas, recombinant
 PT MAGE-1 and immunogenic peptide(s)
 PS Claim 12; Page 20; 33pp; English.
 CC A monoclonal antibody directed against the tumour rejection antigen
 CC (MAGE-1) can be used to detect MAGE-1 in samples by standard
 CC immunoassay methods for diagnosis and monitoring of cancer etc. The
 CC monoclonal antibody is designated MA454 and is produced by the
 CC hybridoma deposited as ATCC HB11540. The monoclonal antibody is
 CC specific for MAGE-1, having no reactivity for MAGE-2 or MAGE-3.
 CC Peptide fragments of MAGE-1 (See R80618-20) may be useful as
 CC immunogens for production of the monoclonal antibody and antisera.
 SQ Sequence 14 AA;

Query Match 100.0%; Score 93; DB 15; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.60e-04;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 inftrqrqsegs 14
 Qy 1 INFTRQRPSEGS 14

RESULT 2

ID R70909 standard; Protein; 309 AA.
 AC R70909;
 DT 09-OCT-1995 (first entry)
 DE Human melanoma antigen MAGE-1.
 KW Human melanoma antigen; MAGE-1; vaccines; MAGE associated tumours;
 KW HLA-restricted cytotoxic T-lymphocyte activity.
 OS Homo sapiens.
 PN W09504542-A.
 PD 16-FEB-1995.
 PF 02-AUG-1993; U08721.
 PR 06-AUG-1993; US-103623.
 PA (CYTE-) CYTEL CORP.
 FI Fikes JD, Livingston BD, Sette AD, Sidney JC;
 DR N-PSDB; Q85435.
 PT Human melanoma antigen, MAGE-1, peptide(s) - useful for
 PT stimulating immune response against melanoma
 PS Example 1; Fig 1; 59pp; English.
 CC Q85435 encodes R70909 human melanoma antigen MAGE-1, it was used
 CC to produce the C-terminal MAGE-1 peptides described in R70915 to
 CC R70969. These peptides are useful for defining epitopes that
 CC engender a HLA-restricted cytotoxic lymphocyte activity against
 CC MAGE-1 antigens. Compsns. containing these peptides can be
 CC administered, as a vaccine to patients susceptible to MAGE
 CC associated tumours, e.g. melanomas.
 SQ Sequence 309 AA;

Query Match 100.0%; Score 93; DB 13; Length 309;
 Best Local Similarity 100.0%; Pred. No. 3.60e-04;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 68 inftrqrqsegs 81
 Qy 1 INFTRQRPSEGS 14

RESULT 3

ID R50092 standard; Protein; 909 AA.
 AC R50092;
 DT 26-OCT-1994 (first entry)
 DE Humanised anti-CEA sFv fragment-human beta-glucuronidase fusion
 DE protein.
 KW Carcinoembryonic antigen; single chain variable region; sFv fragment;
 KW fusion gene; cancer treatment; targetted drug delivery; tumour.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /label= signal peptide
 FT Protein 20..909
 FT /label= fusion protein
 FT /note= "humanised anti-CEA sFv fragment fused to
 FT human beta-glucuronidase"
 PN EP-590350-A.
 PD 06-APR-1994.
 PF 24-SEP-1993; 115418.
 PR 02-OCT-1992; DE-233152.
 PA (BEHW) BEHRINGERWERKE AG.
 FI Boslet K, Czech J, Gehrman M, Seemann G;
 DR WPI; 94-111012/14.
 DR N-PSDB; Q58896.
 PT New fusion protein contg. enzyme for prodrug activation - coupled
 PT to antigen binding component, esp. sFv antibody fragment, partic.
 PT for treatment of tumours
 PS Claim 13; Page 12-15; 35pp; German.
 CC The sequence R50092 comprises a humanised sFv-fragment against CEA
 CC fused to a human beta-glucuronidase. The fusion protein is
 CC useful for targeting beta-glucuronidase to cancer cells expressing
 CC CEA, where the enzyme is able to convert a prodrug into its active
 CC form. Any fusion protein not bound to tumour can be removed by
 CC internalisation via the mannose-6-phosphate and galactose receptors.
 SQ Sequence 909 AA;

Query Match 61.3%; Score 57; DB 10; Length 909;
 Best Local Similarity 63.6%; Pred. No. 8.95e+00;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 867 ftrgrqpkxaa 877
 Qy 3 FTRQRPSEGS 13

RESULT 4

ID P81863 standard; protein; 96 AA.
 AC P81863;
 DT 16-DEC-1990 (first entry)
 DE Sequence encoded by LAV MA L R gene
 KW HIV; HTLV III; AIDS; diagnosis; vaccine; probe; hybridisation.
 OS Lymphadenopathy associated virus MA L.
 PN W08707906-A.
 PD 30-DEC-1987.
 PF 22-JUN-1987; E00326.
 PR 23-JUN-1986; EP-401380.
 PA (INSP) Inst Pasteur.
 PI Alizon M, Sonigo P, Wain-Hobson S, Montagnier L;
 DR WPI; 88-014396/02.
 DR N-PSDB; N80437.

PT New variants of lymphadenopathy associated virus (LAV) -
 PT used for prodn. of DNA, antigens and antibodies used in
 PT diagnosis of AIDS and pre-AIDS
 PS Claim 8; Fig 8A-8I; 72pp; English.
 CC LAV EL I (N80436) and LAV MA 1 (N80437) were isolated from the peripheral
 CC blood lymphocytes of patients. Different AIDS virus isolates concerned
 CC are designated by 3 letters of the patients name. Stable probes including
 CC the DNA sequences can be used for detection of the new LAV viruses or
 CC related viruses or DNA proviruses in eg. biological samples. The proteins
 CC or peptides can be used for detection of antibodies induced in vivo and
 CC present in biological fluids. The DNA can also be used for the expression
 CC of LAV viral antigens for the prodn. of a vaccine against LAV. The
 CC polypeptides can also be used for the prodn. of antibodies for the
 CC detection of proteins related to the LAV viruses, partic. for diagnosis
 CC of AIDS or pre-AIDS.
 SQ Sequence 96 AA;

Query Match 59.1%; Score 55; DB 1; Length 96;
 Best Local Similarity 57.1%; Pred. No. 1.51e+01;
 Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 81 igitrrrarrngas 94
 | : ||||| : |||
 QY 1 INFTRQRPSEGS 14

RESULT 5

ID R65121 standard; peptide; 9 AA.
 AC R65121;
 DT 09-OCT-1995 (first entry)
 DE MAGE 1 immunogenic peptide 66-74.
 KW MAGE 1; immunogenic peptide 66-74; cytotoxic C cells;
 KW in vitro activation; cancer; AIDS; bacterial infections; malaria;
 KW fungal infections; tuberculosis; hepatitis.
 OS Homo sapiens.
 PN WQ9504817-A.
 PD 16-FEB-1995.
 PF 01-AUG-1994; 008672.
 PR 06-AUG-1993; US-103401.
 PA (CYTE-) CYTEL CORP.
 PI Celis E, Kubo R, Serra H, Tsai V, Wentworth P;
 DR WPI; 95-090895/12.
 PT In vitro activation of cytotoxic T cells for selected killing of
 PT target cells - for treating e.g. cancer, AIDS, hepatitis etc.by
 PT incubating them with antigen presenting cells loaded with
 PT appropriate immunogenic peptide
 PS Example 3; Page 35; 53pp; English.
 CC R65109-R65145 are immunogenic peptides, they are used in a new
 CC method for the in vitro activation of cytotoxic T cells (CTC).
 CC This is achieved by incubating the CTCs with antigen presenting
 CC cells loaded with an appropriate immunogenic peptide (e.g. one
 CC of the above peptides). By selecting the peptides used the
 CC following diseases and infections can be treated; cancer, AIDS,
 CC hepatitis, other viral and bacterial infections, malaria and
 CC tuberculosis.
 SQ Sequence 9 AA;

Query Match 57.0%; Score 53; DB 13; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.53e+01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 3 inftrqr 9
 | |||||
 QY 1 INFTRQR 7

RESULT 6

ID R12258 standard; Protein; 96 AA.
 AC R12258;
 DT 20-AUG-1991 (first entry)
 DE HIV-1 strain OYI open reading frame (ORF) R protein.
 DE HIV-1; AIDS; retroviruses.
 KW Homo sapiens.
 OS US5019510-A.
 PN 28-MAY-1991.
 PD 28-OCT-1987; 113655.
 PF 28-OCT-1987; US-113655.
 PR (INSP) INST PASTEUR.
 PA Wain-Hobson S, Huet T, Delaporte E, Brun-Vezinet F;
 DR WPI; 91-177518/24.
 PT Purified human retrovirus - is mutant of HIV-1 having
 PT characteristics of HIV-1 OYI, used in diagnosis of HIV infection
 PS Disclosure; fig 4; 23pp; English.
 CC This sequence constitutes the ORF R protein constituent of a new
 CC strain of HIV-1 retrovirus, OYI. This mutant retroviral strain is
 CC useful in an assay for diagnosing HIV infection. See also Q11943
 CC (OYI nucleotide sequence), R12255-57 and R12259-62 (other HIV OYI
 CC constituent proteins).
 SQ Sequence 96 AA;

Query Match 57.0%; Score 53; DB 3; Length 96;
 Best Local Similarity 50.0%; Pred. No. 2.53e+01;
 Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 81 igitrrrarrngas 94
 | : ||||| : |||
 QY 1 INFTRQRPSEGS 14

RESULT 7

ID R95054 standard; Protein; 342 AA.
 AC R95054;
 DT 19-AUG-1996 (first entry)
 DE TGF-a-DETA-DGAL4 multidomain protein.
 DE Nucleic acid transfer system; gene transfer; gene therapy;
 KW cell targeting; multidomain protein; vector; cancer;
 KW exotoxin A; DETA; ompA; signal peptide; GAL4; TGF-a;
 KW transforming growth factor-alpha.
 OS Chimeric synthetic;
 OS Chimeric Homo sapiens;
 OS Chimeric Pseudomonas aeruginosa;
 OS Chimeric Saccharomyces cerevisiae.
 FH Key Location/Qualifiers
 FT Peptide 1..8
 FT /label= FLAG_epitope
 FT Peptide 9..12
 FT /label= Spacer
 FT Domain 13..62
 FT /label= TGF-a
 FT /note= "amino acids 1-50 of human TGF-a"

FT Peptide 63..65
FT /label= Spacer
FT Peptide 66..71
FT /label= Hexa-histidine
FT Peptide 72
FT /label= Spacer
FT Domain 73..187
FT /label= ETA
FT /note= amino acids 252-366 of ETA"
FT Peptide 188
FT /label= Spacer
FT Domain 189..334
FT /label= GAL4
FT /note= "amino acids 2-147 of yeast GAL4"
FT Peptide 335..342
FT /label= Spacer
FT /note= "endoplasmic reticulum retention signal"
PN W09613599-A1.
PD 09-MAY-1996. E04270.
PF 31-OCT-1995; E04270.
PR 01-NOV-1994; EP-810627.
PA (WELLS/) WELLS W.
PI Fominaya J, Wells W;
DR WPI: 96-239505/24.
DR N-PSDB; T29409.
PT Nucleic acid transfer system for gene therapy, e.g. against cancer
PT - includes toxin translocation domain to target nucleic acid to
PT specific cell
PS Claim 7; Page 64-65; 106pp; English.
CC A multidomain protein (R95054) has a FLAG epitope, a portion
CC of human transforming growth factor-alpha (TGF-a) that acts as a
CC ligand domain, a non-cytotoxic portion of Pseudomonas aeruginosa
CC exotoxin A acting as a translocation domain and the DNA
CC binding domain of yeast GAL4. It is the product of a fusion
CC gene (T29410) and can be expressed in E. coli (resulting in
CC removal of an ompA signal peptide). It is used with an effector
CC nucleic acid that comprises e.g. a gene to be delivered to
CC a cell and a cognate structure for the GAL4 DNA binding domain.
CC This provides a novel means of nucleic acid transfer, suitable
CC for gene therapy.
SQ Sequence 342 AA;

Query Match 57.0%; Score 53; DB 17; Length 342;
Best Local Similarity 85.7%; Pred. No. 2.53e+01;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 93 ftrhrqp 99
QY 3 FTRQRQP 9

RESULT 8
ID R36807 standard; Protein; 414 AA.
AC R36807;
DT 25-AUG-1993 (first entry)
DE Pseudomonas exotoxin domains I and II encoded by pVC-PEBT.
KW Vaccine; cytotoxic T lymphocyte; CTL; influenza A virus;
KW matrix protein; Ma; Pseudomonas exotoxin; cell recognition domain;
OS translocation domain; anti-viral agent.
Pseudomonas aeruginosa.

PN EP-541335-A.
PD 12-MAY-1993.
PF 04-NOV-1992; 310067.
PR 08-NOV-1991; US-792507.
PA (MERI) MERCK & CO INC.
PI Donnelly JJ, Friedman A, Howe LA, Liu MA, Marshall MS;
PI Montgomery DL, Oliff AI, Shi X, Ulmer J;
DR WPI: 93-154266/19.
DR N-PSDB; Q41715.
PT Recombinant DNA encoding bacterial toxin-antigen conjugates - are
PT useful as vaccines against viral infections, tumours and
PT parasites
PS Example 5; Page 30-32; 81pp; English.
CC Control plasmid pVC-PEBT encodes a T7 promoter-driven gene fusion
CC consisting of PE amino acids 2-414 followed by termination codons,
CC instead of by at least part of the influenza A virus Matrix
CC protein (as in e.g. Q41714).
SQ Sequence 414 AA;

Query Match 57.0%; Score 53; DB 7; Length 414;
Best Local Similarity 85.7%; Pred. No. 2.53e+01;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 273 ftrhrqp 279
QY 3 FTRQRQP 9

RESULT 9
ID R32455 standard; Protein; 414 AA.
AC R32455;
DT 20-JUL-1993 (first entry)
DE PE amino acids 2-414.
KW PE; Pseudomonas exotoxin; influenza A virus; M1; matrix protein;
KW T7 polymerase; fusion; hybrid; pVC-PEBT; pVC-PEM1-2.
OS Synthetic.
PN EP-532090-A.
PD 17-MAR-1993.
PF 02-SEP-1992; 202660.
PR 09-SEP-1991; US-756249.
PA (MERI) MERCK & CO INC.
PI Donnelly JJ, Friedman A, Howe LA, Liu MA, Marshall MS;
PI Montgomery DL, Oliff AI, Shi X, Ulmer J;
DR WPI: 93-087107/11.
DR N-PSDB; Q37108.
PT Bacterial toxin-antigen protein conjugates - to elicit cytotoxic
PT T-lymphocyte immune response, used for preventing viral
PT infections, e.g. by influenza virus, HIV and human
PT papilloma: virus
PS Disclosure; Page 33-35; 83pp; English.
CC Example 5 describes the construction of pVC-PEBT.
CC A control plasmid was constructed which encodes a T7 polymerase
CC driven gene fusion consisting of PE amino acids 2 to 414 followed by
CC termination codons. pVC-PEM1-2 was digested with SacII and EcoRI to
CC remove the M1 sequence. The vector was gel purified and ligated to
CC an oligonucleotide that builds back PE codon no. 414 followed by
CC termination signals shown in Q37893. The resulting construction
CC was named pVC-PEBT (Q37108).
SQ Sequence 414 AA;

Query Match 57.0%; Score 53; DB 7; Length 414;
Best Local Similarity 85.7%; Pred. No. 2.53e+01;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 273 ftrhrqp 279
|||||
Qy 3 FTRQRQP 9

RESULT 10

ID R07054 standard; protein; 419 AA.
AC R07054;
DT 18-JAN-1991 (first entry)
DE PE40AB protein comprising a portion of the Pseudomonas exotoxin A.
KW TGF-alpha-PE40; PE40ab; tumour; epidermal growth factor; EGF;
KW transforming growth factor-alpha; TGF-alpha.
OS Pseudomonas sp.
PN EP-389043-A.
PD 26-SEP-1990.
PF 15-MAR-1990; 200613.
PR 22-MAR-1989; US-327214.
PA (MERI) MERCK & CO INC.
PI Riemen MW, Stirdivant SM;
DR WPI; 90-291988/39.
DR N-PSDB; Q06127.
PT Modified PE40 by substitution with other amino acids for cysteine -
PT improving specificity of targeting agent for tumour cells.
PS Disclosure; Table 3; 21pp; English.
CC By replacing cysteine residues at positions 265 and 287 and/or 372
CC and 379, chemical ambiguities may be eliminated, and targeting
CC specificity for targeted agents of tumour cells eg. EGF or TGF-alpha
CC may be improved.
SQ Sequence 419 AA;

Query Match 57.0%; Score 53; DB 2; Length 419;
Best Local Similarity 85.7%; Pred. No. 2.53e+01;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 79 ftrhrqp 85
|||||
Qy 3 FTRQRQP 9

RESULT 11

ID R06447 standard; protein; 420 AA.
AC R06447;
DT 04-JAN-1991 (first entry)
DE TGF-57-Pseudomonas exotoxin 40 fusion protein.
KW Pseudomonas exotoxin-40 (PE40); protein targeting agent;
KW psoriasis treatment; anti-tumour agent;
FH Key Location/Qualifiers
FT Region 1..54
FT /label=residues -4 to +50 of TGF-alpha
FT Region 58..420
FT /label=residues +252 to +613 of PE
PN EP-383599-A.
PD 22-AUG-1990.
PF 15-FEB-1990; 301639.
PR 17-FEB-1989; US-312540.
PR 03-AUG-1989; US-389092.

PR 21-DEC-1989; US-449187.
PA (MERI) MERCK & CO INC.
PI Oliff A, Jones DD, Edwards GM;.
DR WPI; 90-255832/34.
DR N-PSDB; Q05666.

PT Modified pseudomonas exotoxin hybrid proteins - has at least 2
PT cysteine residues replaced or deleted to improve binding to
PT receptors.
PS Example; Table 2; 20pp; English.
CC Modified pseudomonas exotoxin (PE40) linked to
CC 5' portion of transforming growth factor (TGF)-alpha as a targeting
CC agent. The corresponding nucleotide sequence was constructed from
CC a synthetic oligonucleotide encoding the 5' portion of TGF-alpha
CC and linked to PE40 and a linker cassette called "cassette 57". The
CC recombinant plasmid was used to transform E.coli JM109 cells.
CC The hybrid protein can bind and kill tumour cells or keratinocytes
CC possessing TGF receptors for treatment of psoriasis or warts.
CC See also R06448-R06450
SQ Sequence 420 AA;

Query Match 57.0%; Score 53; DB 2; Length 420;
Best Local Similarity 85.7%; Pred. No. 2.53e+01;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 79 ftrhrqp 85
|||||
Qy 3 FTRQRQP 9

RESULT 12

ID R06993 standard; protein; 420 AA.
AC R06993;
DT 18-JAN-1991 (first entry)
DE PE40AB protein comprising a portion of the Pseudomonas exotoxin A
DE lacking cysteine residues at 372 and 379.
KW TGF-alpha-PE40; PE40ab; tumour; epidermal growth factor; EGF;
KW transforming growth factor-alpha; TGF-alpha.
OS Pseudomonas sp.
PN EP-389043-A.
PD 26-SEP-1990.
PF 15-MAR-1990; 200613.
PR 22-MAR-1989; US-327214.
PA (MERI) MERCK & CO INC.
PI Riemen MW, Stirdivant SM;
DR WPI; 90-291988/39.
PT Modified PE40 by substitution with other amino acids for cysteine -
PT improving specificity of targeting agent for tumour cells.
PS Disclosure; Table 5; 21pp; English.
CC By replacing cysteine residues at positions 265 and 287 and/or 372
CC and 379, chemical ambiguities may be eliminated, and targeting
CC specificity for targeted agents of tumour cells eg. EGF or TGF-alpha
CC may be improved.
CC See also Q06127.
SQ Sequence 420 AA;

Query Match 57.0%; Score 53; DB 2; Length 420;
Best Local Similarity 85.7%; Pred. No. 2.53e+01;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 79 ftrhrqp 85

Qy
3 FTRQRQ 9
||||:||||

RESULT 13
ID R20200 standard; Protein; 420 AA.
AC R20200;
DT 16-APR-1992 (first entry)
DE TGF-alpha-PE40Ab.
KW Pseudomonas exotoxin; bladder; mutant; target; receptor binding.
FH Key Location/Qualifiers
FT Region 5..54
FT /label= TGFalpha1-50
FT Region 59..420
FT /label= PE252-613
FT Misc difference 176
FT /note= "Ser -> Thr"
FT Misc difference 179
FT /note= "Cys -> Ala"
FT Misc difference 186
FT /note= "Cys -> Ala"
FN EP-467536-A.
PD 22-JAN-1992.
PF 20-JUN-1991; US-542281.
PR 21-JUN-1990; US-542281.
PR 14-MAR-1991; US-669269.
PA (MERI) MERCK & CO INC.
PI Ahern J, Heimbrook DC, Oliff AI, Stirdivant SM;
DR WPI; 92-026359/04.
PT Treatment of bladder cancer using hybrid protein - comprising
PT cell targeting agent e.g. EGF that binds to EGF receptor on
PT tumour cells and PE40 cell toxin
PS Disclosure; Page 18-19; 34pp; English.
CC The modified PE40 domains of the hybrid proteins have two or four of
CC the Cys residues (designated Cys265, Cys287, Cys372 and Cys372)
CC substituted with neutral amino acids, e.g. Gly, Ala, or Phe.
CC TGF-alpha-PE40Ab (R20199) has Cys265 and Cys287 replaced; and
CC TGF-alpha-PE40Ab (R20200) has Cys372 and Cys379 replaced; and
CC TGF-alpha-PE40Ab (R20201) has all four replaced.
CC The modified hybrid proteins were produced in E.coli transformed
CC with TAC expression vectors. Site specific mutations were introduced
CC to the unmodified TGF-alpha-PE40 gene cloned in pTACTCF57-PE40.
CC The mol. efficiently targets receptors on human bladder tumour cells
CC (the modified PE40 domain has improved receptor binding) and is
CC used for selectively killing bladder tumour cells.
SQ Sequence 420 AA;

Query Match 57.0%; Score 53; DB 4; Length 420;
Best Local Similarity 85.7%; Pred. No. 2.53e+01;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 79 ftrhrqp 85
||||:||||
Qy 3 FTRQRQ 9

RESULT 14
ID R06449 standard; protein; 420 AA.
AC R06449;
DT 04-JAN-1991 (first entry)

DE TGF-alpha-PE40-Ab modified pseudomonas exotoxin hybrid protein.
KW Pseudomonas exotoxin-40 (PE40); protein targeting agent;
KW psoriasis treatment; anti-tumour agent; TGF-alpha-PE40-Ab;
FH Key Location/Qualifiers
FT Region 1..54
FT /label= residues -4 to +50 of TGF-alpha
FT Region 58..420
FT /label= residues +252 to +613 of PE
FT /notes= residues 369, 372 and 379 are modified"
PN EP-383599-A.
PD 22-AUG-1990.
PF 15-FEB-1990; 301639.
PR 17-FEB-1989; US-312540.
PR 03-AUG-1989; US-389092.
PR 21-DEC-1989; US-449187.
PA (MERI) MERCK & CO INC.
PI Oliff A, Jones DD, Edwards GM;
DR WPI; 90-255832/34.
PT Modified pseudomonas exotoxin hybrid proteins - has at least 2
PT cysteine residues replaced or deleted to improve binding to
PT receptors.
PS Example ; Table 5; 20pp; English.
CC Modified pseudomonas exotoxin (PE40) linked to
CC 5' portion of transforming growth factor (TGF)-alpha as a targeting
CC agent. Three site-specific mutations have been introduced c.f wild-
CC type PE40. The Cys residues at positions 369 and 379 of the
CC exotoxin have been replaced by Ala residues. Ser at position 369
CC has been replaced with Thr. These changes improve receptor binding.
CC The hybrid protein can bind and kill tumour cells or keratinocytes
CC possessing TGF receptors for treatment of psoriasis or warts.
CC See also R06447-R06448 and R06450
SQ Sequence 420 AA;

Query Match 57.0%; Score 53; DB 2; Length 420;
Best Local Similarity 85.7%; Pred. No. 2.53e+01;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 79 ftrhrqp 85
||||:||||
Qy 3 FTRQRQ 9

RESULT 15
ID R95055 standard; Protein; 421 AA.
AC R95055;
DT 19-AUG-1996 (first entry)
DE IL-2-DETA-DGAL4 multidomain protein.
KW Nucleic acid transfer system; gene transfer; gene therapy;
KW cell targeting; multidomain protein; vector; cancer;
KW exotoxin A; DETA; ompA; signal peptide; GAL4; interleukin-2;
KW IL-2.
OS Chimeric synthetic;
OS Chimeric Homo sapiens;
OS Chimeric Pseudomonas aeruginosa;
OS Chimeric Saccharomyces cerevisiae;
FH Key Location/Qualifiers
FT Peptide 1..8
FT /label= FLAG epitope
FT Peptide 9..17
FT /label= Spacer

```

FT Domain 18..150
FT /label= IL-2
FT /note= "amino acids 1-113 of human IL-2"
FT Peptide 151
FT /label= Spacer
FT Domain 152..266
FT /label= ETA
FT /note= "amino acids 252-366 of ETA"
FT Peptide 267
FT /label= Spacer
FT Domain 268..413
FT /label= GAL4
FT /note= "amino acids 2-147 of yeast GAL4"
FT Peptide 414..421
FT /label= Spacer
FT /note= "endoplasmic reticulum retention signal"
FT /note= "endoplasmic reticulum retention signal"
PN W09613599-A1.
PD 09-MAY-1996.
PF 31-OCT-1995; E04270.
PR 01-NOV-1994; EP-810627.
PA (WELLS) WELLS W.
PI Fominaya J, Wells W;
DR WPI; 96-239505/24.
DR N-PSDB; T29411.
PT Nucleic acid transfer system for gene therapy, e.g. against cancer
PT - includes toxin translocation domain to target nucleic acid to
PT specific cell
PS Claim 7; Page 67-69; 106pp; English.
CC A multidomain protein (R95055) has a FLAG epitope, a portion
CC of human interleukin-2 that acts as a ligand domain, a
CC non-cytotoxic portion of Pseudomonas aeruginosa exotoxin A acting
CC as a translocation domain and the DNA binding domain of yeast GAL4.
CC It is the product of a fusion gene (T29411) and can be expressed
CC in E. coli (resulting in removal of an ompA signal peptide). It is
CC used with an effector nucleic acid that comprises e.g. a gene to be
CC delivered to a cell and a cognate structure for the GAL4 DNA binding
CC domain. This provides a novel means of nucleic acid transfer,
CC suitable for gene therapy.
SQ Sequence 421 AA;

```

Query Match 57.0%; Score 53; DB 17; Length 421;
 Best Local Similarity 85.7%; Pred. No. 2.53e+01;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 172 ftrhrqp 178

Qy 3 FTRQRQP 9

Search completed: Thu Apr 3 11:57:35 1997
 Job time : 8 secs.

W09613599-A1

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Apr 3 11:56:58 1997; MasPar time 2.60 Seconds
 138.323 Million cell updates/sec

Tabular output not generated.

Title: >US-08-190-411A-2
 Description: (1-14) from 5541104.pep
 Perfect Score: 93
 Sequence: 1 INFTQRQPFSEGS 14

Scoring table: PAM 150
 Gap 15

Searched: 82182 seqs, 25727515 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: pir48
 1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4
 8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unann
 14:unrev

Statistics: Mean 24.209; Variance 34.429; scale 0.703

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description	Pred. No.
1	93	100.0	280	12	JC2358 tumor-associated ant	2.39e-08
2	60	64.5	184	7	I39725 ORF14 - Agrobacteriu	3.04e-01
3	57	61.3	317	12	JC2359 tumor-associated ant	1.13e+00
4	57	61.3	651	4	A26381 beta-glucuronidase (1.13e+00
5	56	60.2	56	4	A35798 beta-glucuronidase (1.74e+00
6	56	60.2	648	4	B32576 beta-glucuronidase (1.74e+00
7	56	60.2	648	4	A32576 beta-glucuronidase (1.74e+00
8	56	60.2	648	4	A29977 beta-glucuronidase (1.74e+00
9	55	59.1	96	7	S54380 vpr protein - human	2.67e+00
10	55	59.1	1703	10	SI5047 SNF2 protein - yeast	2.67e+00
11	54	58.1	186	14	S46450 hypothetical protein	4.06e+00
12	53	57.0	167	8	B53293 flm3 region hypotet	6.16e+00
13	53	57.0	638	7	A30347 exotoxin A precursor	6.16e+00
14	50	53.8	330	6	B60816 major iron-regulated	2.08e+01
15	50	53.8	330	6	SI0256 iron-binding protein	2.08e+01
16	50	53.8	410	11	A48585 transcription factor	2.08e+01
17	50	53.8	793	1	SURFCA ATP-dependent Clp pr	2.08e+01

```
18 50 53.8 889 6 A41259 potassium transport 2.08e+01
19 49 52.7 128 1 NRYV pancreatic ribonucle 3.08e+01
20 49 52.7 130 5 S03523 T-cell receptor alph 3.08e+01
21 49 52.7 237 12 A48912 leucine zipper prote 3.08e+01
22 49 52.7 349 7 A28658 nitrilase (EC 3.5.5. 3.08e+01
23 49 52.7 494 8 A47059 sucrose ScrB - Staph 3.08e+01
24 49 52.7 542 10 JQ1524 O-succinylhomoserine 3.08e+01
25 49 52.7 648 4 A25047 beta-glucuronidase ( 3.08e+01
26 48 51.6 94 2 R3PU19 ribosomal protein SI 4.54e+01
27 48 51.6 220 6 S35789 US2 protein - bovine 4.54e+01
28 48 51.6 272 7 C32058 mcbC protein - Esche 4.54e+01
29 48 51.6 518 10 S42387 MPP protein homolog 4.54e+01
30 48 51.6 551 14 S03667 homeotic protein eng 4.54e+01
31 48 51.6 552 3 WJFFEN homeotic protein eng 4.54e+01
32 48 51.6 584 6 B25682 homeotic protein Eng 4.54e+01
33 48 51.6 3573 8 S23070 6-deoxyerythronolide 4.54e+01
34 47 50.5 159 12 A48428 murine clone MH-1 pr 6.65e+01
35 47 50.5 231 1 RDNGUF ubiquinol--cytochrom 6.65e+01
36 47 50.5 305 11 S22313 YB3 protein - Africa 6.65e+01
37 47 50.5 321 12 S22822 transcription factor 6.65e+01
38 47 50.5 322 12 A45976 MSY1 protein - mouse 6.65e+01
39 47 50.5 322 12 A23677 transcription factor 6.65e+01
40 47 50.5 324 11 I39382 dbpB homolog BP-8 - 6.65e+01
41 47 50.5 324 12 A55971 major core protein p 6.65e+01
42 47 50.5 527 4 S13763 protein-tyrosine kin 6.65e+01
43 47 50.5 602 4 JU0215 tyrosine kinase, tec 6.65e+01
44 47 50.5 630 4 JU0228 protein tyrosine kin 6.65e+01
45 47 50.5 1359 10 S49883 nuclear protein STH1 6.65e+01
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ALIGNMENTS

```
1
RESULT JC2358 #type complete
ENTRY tumor-associated antigen , MAGE-1 - human
TITLE #formal name Homo sapiens #common name man
ORGANISM 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
DATE 15-Mar-1996

ACCESSIONS JC2358
REFERENCE JC2358
#authors Ding, M.; Beck, R.J.; Keller, C.J.; Fenton, R.G.
#journal Biochem. Biophys. Res. Commun. (1994) 202:549-555
#title Cloning and analysis of MAGE-1-related genes.
#accession JC2358
#molecule type mRNA
#residues 1-280 #label DIN
#experimental_source melanoma cell line DM150

GENETICS MAGE
#gene
FEATURE
161-169 #region HLA-A1 binding #status predicted
SUMMARY #length 280 #molecular-weight 30932 #checksum 467

Query Match 100.0%; Score 93; DB 12; Length 280;
Best Local Similarity 100.0%; Pred. No. 2.38e-08;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 68 inftrqrpsqgs 81
| | | | | | | | | |
Qy 1 INFTRQRPSEGS 14
```

```
2
RESULT I39725 #type complete
ENTRY ORF14 - Agrobacterium rhizogenes plasmid pRI8196
TITLE #formal name Agrobacterium rhizogenes
ORGANISM 09-Mar-1996 #sequence_revision 09-Mar-1996 #text_change
DATE 09-Mar-1996

ACCESSIONS I39725
REFERENCE I39720
#authors Hansen, G.; Larribe, M.; Vaubert, D.; Tempe, J.; Biermann,
B.J.; Montoya, A.L.; Chilton, M.
#journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:7763-7767
#title Agrobacterium rhizogenes pRI8196 T-DNA: Mapping and DNA
sequence of functions involved in mannopine synthesis and
hairy root differentiation.
#cross-references M01D:91352070
#accession I39725
#status preliminary
#molecule_type DNA
#residues 1-184 #label RES
#cross-references GB:M60490; NID:gl42245; CDS_PID:gl42251

GENETICS
#genome plasmid
#note encoded within the T-DNA (transferred DNA) segment of the
plasmid; this segment integrates stably into the host
genome, stimulates mannopine synthesis and root formation,
and causes hairy root disease
#length 184 #molecular-weight 20254 #checksum 2851

SUMMARY
```

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Query Match 64.5%; Score 60; DB 7; Length 184;
Best Local Similarity 72.7%; Pred. No. 3.04e-01;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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Db 157 ftrqrqpdqs 167
| | | | | | | |
Qy 3 FTRQRPSEGS 13
```

```
3
RESULT JC2359 #type complete
ENTRY tumor-associated antigen , MAGE-X2 - human
TITLE #formal name Homo sapiens #common name man
ORGANISM 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
DATE 15-Mar-1996

ACCESSIONS JC2359
REFERENCE JC2358
#authors Ding, M.; Beck, R.J.; Keller, C.J.; Fenton, R.G.
#journal Biochem. Biophys. Res. Commun. (1994) 202:549-555
#title Cloning and analysis of MAGE-1-related genes.
#accession JC2359
#molecule type mRNA
#residues 1-317 #label DIN
#experimental_source melanoma cell line DM150

GENETICS MAGE-X2
#gene
FEATURE
169-177 #region HLA-A1 binding #status predicted
SUMMARY #length 317 #molecular-weight 34928 #checksum 9004
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Query Match      61.3%; Score 57; DB 12; Length 317;
Best local Similarity 71.4%; Pred. No. 1.13e+00;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 76 jsfctwqpnegs 89
QY 1 INFTRQRPSEGSS 14
      1:111 111:1111
      1 INFTRQRPSEGSS 14

RESULT 4
ENTRY
TITLE      A26581      #type complete
ORGANISM   beta-glucuronidase (EC 3.2.2.1.31) precursor - human
DATE       05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change
          01-Mar-1996

ACCESSIONS
REFERENCE  A26581; A40337; A24983; A36538
AUTHORS    Oshima, A.; Kyle, J.W.; Miller, R.D.; Hoffmann, J.W.; Powell,
            P.P.; Grubb, J.H.; Sly, W.S.; Tropak, M.; Guise, K.S.;
            Gravel, R.A.
JOURNAL    Proc. Natl. Acad. Sci. U.S.A. (1987) 84:685-689
TITLE      Cloning, sequencing, and expression of cDNA for human
            beta-glucuronidase.
CROSS-REFERENCES MUID:87118233
ACCESSION  A26581
            #molecule_type mRNA
            #residues 1-651 #label OSH
            ##experimental_source placenta
REFERENCE  A40337
AUTHORS    Shipley, J.M.; Miller, R.D.; Wu, B.M.; Grubb, J.H.;
            Christensen, S.G.; Kyle, J.W.; Sly, W.S.
JOURNAL    Genomics (1991) 10:1009-1018
TITLE      Analysis of the 3' flanking region of the human
            beta-glucuronidase gene.
CROSS-REFERENCES MUID:92009900
ACCESSION  A40337
            #molecule_type DNA
            #residues 1-70 #label SHI
            ##cross-references GB:M65002
REFERENCE  A24983
AUTHORS    Guise, K.S.; Korneluk, R.G.; Wayne, J.; Lambonwah, A.M.; Quan,
            F.; Palmer, R.; Ganschow, R.E.; Sly, W.S.; Gravel, R.A.
JOURNAL    Gene (1985) 34:105-110
TITLE      beta-glucuronidase gene.
CROSS-REFERENCES MUID:85232043
ACCESSION  A24983
            #molecule_type mRNA
            #residues 520-585 #label GUI
REFERENCE  A36538
AUTHORS    Tomatsu, S.; Fukuda, S.; Sukegawa, K.; Ikedo, Y.; Yamada, S.;
            Yamada, Y.; Sasaki, T.; Okamoto, H.; Kuwahara, T.;
            Yamaguchi, S.; Kiman, T.; Shintaku, H.; Ishiki, G.; Orii,
            T.
JOURNAL    Am. J. Hum. Genet. (1991) 48:89-96
TITLE      Mucopolysaccharidosis type VII: characterization of mutations
            and molecular heterogeneity.
CROSS-REFERENCES MUID:91090114
ACCESSION  A36538
            #molecule_type mRNA
            #residues 378-385, 616-621, 643-651 #label TOM
GENETICS

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#gene	GDB:CUSB
#cross-references	GDB:G00-120-025
#map_position	7q22
CLASSIFICATION	#superfamily beta-glucuronidase
KEYWORDS	glycoprotein; glycosidase; homotetramer; hydrolase; lysosome
FEATURE	
1-22	#domain signal sequence #status predicted #label SIG\
23-651	#product beta-glucuronidase, placental #status predicted
SUMMARY	#label MAT
	#length 651 #molecular-weight 74715 #checksum 1663
Query Match	61.3%; Score 57; DB 4; Length 651;
Best Local Similarity	63.6%; Pred.No. 1.13e+00;
Matches	7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Db	609 ftrqrpkpsaa 619
QY	3 FTRQRPSEGS 13
	::
RESULT	5
ENTRY	A35798
TITLE	#type fragment
ORGANISM	beta-glucuronidase (EC 3.2.1.31) - mouse (fragment)
DATE	#formal name Mus musculus #common name house mouse
	23-Oct-1990 #sequence_revision 23-Oct-1990 #text_change
	23-Jun-1993
ACCESSIONS	A35798
REFERENCE	A35798
#authors	Li, H. i Takeuchi, K.H.; Manly, K.; Chapman, V.; Swank, R.T.
#journal	J. Biol. Chem. (1990) 265:14732-14735
#title	The propeptide of beta-glucuronidase. Further evidence of its involvement in compartmentalization of beta-glucuronidase and sequence similarity with portions of the reactive site region of the serpin superfamily.
#cross-references	MUID:90368633
#accession	A35798
#status	preliminary; not compared with conceptual translation
#molecule_type	mRNA
#residues	1-56 #label LIA
CLASSIFICATION	#superfamily beta-glucuronidase
KEYWORDS	glycosidase; hydrolase
SUMMARY	#length 56 #checksum 2307
Query Match	60.2%; Score 56; DB 4; Length 56;
Best Local Similarity	100.0%; Pred.No. 1.74e+00;
Matches	7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	13 ftrqrpk 19
QY	3 FTRQRP 9
	::
RESULT	6
ENTRY	B32576
TITLE	#type complete
ORGANISM	beta-glucuronidase (EC 3.2.1.31) H - mouse
DATE	#formal name Mus musculus #common name house mouse
	12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change
	23-Jun-1993
ACCESSIONS	B32576
REFERENCE	A32576

```

#authors      Wawrzyniak, C.J.; Gallagher, P.M.; D'Amore, M.A.; Carter,
              J.E.; Lund, S.D.; Rinchik, E.M.; Ganschow, R.E.
#journal      Mol. Cell. Biol. (1989) 9:4074-4078
#title        DNA determinants of structural and regulatory variation
              within the murine beta-glucuronidase gene complex.
#cross-references MUID:89384641
#accession    B32576
#status       preliminary
#molecule_type mRNA
#residues     1-648 #label WAW
#cross-references GB:M27816
CLASSIFICATION #superfamily beta-glucuronidase
KEYWORDS       glycosidase; hydrolase
SUMMARY        #length 648 #molecular-weight 74207 #checksum 8794

Query Match      60.2%; Score 56; DB 4; Length 648;
Best Local Similarity 100.0%; Pred. No. 1.74e+00;
Matches          7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 605 ftrqrp 611
| | | | |
Qy 3 FTRQRP 9

RESULT 7
ENTRY   A32576 #type complete
TITLE   beta-glucuronidase (EC 3.2.1.31) B - mouse
ORGANISM #formal name Mus musculus #common name house mouse
DATE     12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change
        23-Jun-1993
ACCESSIONS A32576
REFERENCE  Wawrzyniak, C.J.; Gallagher, P.M.; D'Amore, M.A.; Carter,
           J.E.; Lund, S.D.; Rinchik, E.M.; Ganschow, R.E.
           Mol. Cell. Biol. (1989) 9:4074-4078
           DNA determinants of structural and regulatory variation
           within the murine beta-glucuronidase gene complex.
#cross-references MUID:89384641
#accession    A32576
#status       preliminary
#molecule_type mRNA
#residues     1-648 #label WAW
#cross-references GB:M27816
CLASSIFICATION #superfamily beta-glucuronidase
KEYWORDS       glycosidase; hydrolase
SUMMARY        #length 648 #molecular-weight 74195 #checksum 9124

Query Match      60.2%; Score 56; DB 4; Length 648;
Best Local Similarity 100.0%; Pred. No. 1.74e+00;
Matches          7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 605 ftrqrp 611
| | | | |
Qy 3 FTRQRP 9

RESULT 8
ENTRY   A29577 #type complete
TITLE   beta-glucuronidase (EC 3.2.1.31) precursor - mouse
ALTERNATE_NAMES beta-D-glucuronoside glucuronosohydrolase

```

```

ORGANISM      #formal name Mus musculus #common name house mouse
DATE          19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change
              27-Jun-1994
ACCESSIONS    A28954; A29977
REFERENCE     D'Amore, M.A.; Gallagher, P.M.; Korfhagen, T.R.; Ganschow,
              R.E.
              Biochemistry (1988) 27:7131-7140
              Complete sequence and organization of the murine
              beta-glucuronidase gene.
#cross-references MUID:89062453
#accession    A28954
#molecule_type DNA
#residues     1-648 #label DAM
REFERENCE     A29977
              Gallagher, P.M.; D'Amore, M.A.; Lund, S.D.; Ganschow, R.E.
              Genomics (1988) 2:215-219
              The complete nucleotide sequence of murine beta-glucuronidase
              mRNA and its deduced polypeptide.
#cross-references MUID:88284700
#accession    A29977
#molecule_type mRNA
#residues     1-648 #label GAL
GENETICS      #introns      70/3; 132/3; 193/2; 241/1; 303/3; 351/3; 411/2; 460/2; 488/3;
              547/3; 593/1
CLASSIFICATION #superfamily beta-glucuronidase
KEYWORDS       glycosidase; hydrolase
FEATURE        1-22          #domain signal sequence #label SIG\
              23-648         #product beta-glucuronidase #label MAT
              #length 648 #molecular-weight 74239 #checksum 9468

Query Match      60.2%; Score 56; DB 4; Length 648;
Best Local Similarity 100.0%; Pred. No. 1.74e+00;
Matches          7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 605 ftrqrp 611
| | | | |
Qy 3 FTRQRP 9

RESULT 9
ENTRY   S54380 #type complete
TITLE   vpr protein - human immunodeficiency virus type 1
ORGANISM #formal name human immunodeficiency virus type 1, HIV-1
DATE     15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change
        01-Sep-1995
ACCESSIONS    S54380
REFERENCE     Theodore, T.; Buckler-White, A.J.
              Submitted to the EMBL Data Library, July 1989
              S54377
              submitted to the EMBL Data Library, July 1989
              S54380
              #status       preliminary
              #molecule_type genomic RNA
              #residues     1-96 #label THE
              #cross-references EMBL:M22639
SUMMARY        #length 96 #molecular-weight 11380 #checksum 8538

Query Match      59.1%; Score 55; DB 7; Length 96;

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Best Local Similarity 57.1%; Pred. No. 2.67e+00;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 81 igitrrrrarnges 94
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QY 1 INFTRQRPSEGS 14

RESULT 10
ENTRY S15047 #type complete
TITLE SNF2 protein - yeast (Saccharomyces cerevisiae)
ORGANISM #formal name Saccharomyces cerevisiae
DATE 28-May-1993 #sequence_revision 28-May-1993 #text_change 18-Nov-1994

ACCESSIONS S15047; S16820
REFERENCE S15047
#authors Laurent, B.C.; Treitel, M.A.; Carlson, M.
#journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:2687-2691
#title Functional interdependence of the yeast SNF2, SNF5, and SNF6 proteins in transcriptional activation.
#cross-references M01D:91187857
#accession S15047
#molecule_type DNA
#residues 1-1703 #label PRO
#cross-references EMBL:M61703

REFERENCE S16820
#authors Yoshimoto, H.; Yamashita, I.
#journal Mol. Gen. Genet. (1991) 228:270-280
#title The GAM1/SNF2 gene of Saccharomyces cerevisiae encodes a highly charged nuclear protein required for transcription of the STAL gene.
#cross-references M01D:91360076
#accession S16820
#molecule_type DNA
#residues 1-1703 #label YOS
#cross-references EMBL:X57837

GENETICS
#gene LISTA:SNF2; GAM1
CLASSIFICATION #superfamily bromodomain homology
KEYWORDS nucleus; transcription regulation
FEATURE
1576-1631 #domain bromodomain homology #label BRO
SUMMARY #length 1703 #molecular-weight 194050 #checksum 6560

Query Match 59.1%; Score 55; DB 10; Length 1703;
Best Local Similarity 50.0%; Pred. No. 2.67e+00;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 299 efarrrrptd 308
|:|:|:|:|
QY 2 NFTRQRPSE 11

RESULT 11
ENTRY S46450 #type complete
TITLE hypothetical protein 14 - Tree tobacco
ORGANISM #formal name Nicotiana glauca #common name tree tobacco
DATE 15-Jul-1995 #sequence_revision 15-Jul-1995 #text_change 15-Jul-1995

ACCESSIONS S46450

S46449
Aoki, S.; Kawaoka, A.; Sekine, M.; Ichikawa, T.; Fujita, T.; Shimno, A.; Syono, K.
Mol. Gen. Genet. (1994) 243:706-710
Sequence of the cellular T-DNA in the untransformed genome of Nicotiana glauca that is homologous to ORFs 13 and 14 of the Ri plasmid and analysis of its expression in genetic tumors of N. glauca x N. langsdorffii.

#accession S46450
#status preliminary
#residues 1-186 #label AOK
SUMMARY #length 186 #molecular-weight 20952 #checksum 8973

Query Match 58.1%; Score 54; DB 14; Length 186;
Best Local Similarity 63.6%; Pred. No. 4.06e+00;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 159 ftrghpqdps 169
|:|:|:|:|
QY 3 FTRQRPSEGS 13

RESULT 12
ENTRY B53293 #type complete
TITLE flm3 region hypothetical protein 2 - Synechococcus sp. (PCC 7942)
ORGANISM #formal name Synechococcus sp.
DATE 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 03-Oct-1995

ACCESSIONS B53293
REFERENCE A53293
#authors Dolganov, N.; Grossman, A.R.
#journal J. Bacteriol. (1993) 175:7644-7651
#title Insertional inactivation of genes to isolate mutants of Synechococcus sp. strain PCC 7942: isolation of filamentous strains.
#accession B53293
#status preliminary
#molecule_type DNA
#residues 1-167 #label DOL
#cross-references GB:L19521

GENETICS
#start_codon GTT
SUMMARY #length 167 #molecular-weight 18772 #checksum 1059

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Best Local Similarity 50.0%; Pred. No. 6.16e+00;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 74 vnyarqrqag 83
|:|:|:|:|
QY 1 INFTRQRP 10

RESULT 13
ENTRY A30347 #type complete
TITLE exotoxin A precursor - Pseudomonas aeruginosa
ORGANISM #formal name Pseudomonas aeruginosa
DATE 08-Jun-1990 #sequence_revision 08-Jun-1990 #text_change 30-Sep-1993

ACCESSIONS A30347
REFERENCE A30347
#authors Gray, G.L.; Smith, D.H.; Baldridge, J.S.; Harkins, R.N.;
Vasil, M.L.; Chen, E.Y.; Heyneker, H.L.;
Proc. Natl. Acad. Sci. U.S.A. (1984) 81:2645-2649
#journal Cloning, nucleotide sequence, and expression in Escherichia
#title coli of the exotoxin A structural gene of Pseudomonas
aeruginosa.
#cross-references MUID:84194063
#accession A30347
#status preliminary
#molecule type DNA
#residues 1-638 #label GRA
SUMMARY #length 638 #molecular-weight 69308 #checksum 3979
Query Match 57.0%; Score 53; DB 7; Length 638;
Best Local Similarity 85.7%; Pred. No. 6.16e+00;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 297 fthrdp 303
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Qy 3 FTRQRP 9

RESULT 14 B0816 #type complete
ENTRY major iron-regulated protein - Neisseria meningitidis
TITLE iron-binding protein; MIRP
ALTERNATE_NAMES #formal name Neisseria meningitidis
ORGANISM 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
DATE 31-Dec-1993
ACCESSIONS S10978; B0816
REFERENCE S10978
#authors Berish, S.A.; Kapczynski, D.R.; Morse, S.A.
#journal Nucleic Acids Res. (1990) 18:4596
#title Nucleotide sequence of the fbp gene from Neisseria
meningitidis.
#cross-references MUID:90356404
#accession S10978
#molecule type DNA
#residues 1-330 #label BER
#cross-references EMBL:X53467

REFERENCE A60816
#authors Morse, S.A.; Mietzner, T.A.; Bolen, G.; LeFaou, A.;
Schoolnik, G.
#journal Antonie Van Leeuwenhoek (1987) 53:465-469
#title Characterization of the major iron-regulated protein of
Neisseria gonorrhoeae and Neisseria meningitidis.
#accession B0816
#molecule type protein
#residues 23-69 #label MOR
GENETICS
#gene Fbp
#superfamily sfuA protein
CLASSIFICATION iron binding
KEYWORDS
FEATURE 23-330
#product major iron-regulated protein #status
experimental #label MAT
SUMMARY #length 330 #molecular-weight 35741 #checksum 1589

Query Match 53.8%; Score 50; DB 6; Length 330;
Best Local Similarity 50.0%; Pred. No. 2.08e+01;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 235 Infvhrdpg 244
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Qy 1 INFTRQRP 10

RESULT 15 S10256 #type complete
ENTRY iron-binding protein precursor - Neisseria gonorrhoeae
TITLE major iron-regulated protein Fbp
ALTERNATE_NAMES #formal name Neisseria gonorrhoeae
ORGANISM 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change
DATE 30-Sep-1993
ACCESSIONS S10256; A60816
REFERENCE S10256
#authors Berish, S.A.; Mietzner, T.A.; Mayer, L.W.; Genco, C.A.;
Holloway, B.P.; Morse, S.A.
#journal J. Exp. Med. (1990) 171:1535-1546
#title Molecular cloning and characterization of the structural gene
for the major iron-regulated protein expressed by Neisseria
gonorrhoeae.
#cross-references MUID:90237747
#accession S10256
#molecule type DNA
#residues 1-330 #label BER
#cross-references EMBL:X51901

REFERENCE A60816
#authors Morse, S.A.; Mietzner, T.A.; Bolen, G.; LeFaou, A.;
Schoolnik, G.
#journal Antonie Van Leeuwenhoek (1987) 53:465-469
#title Characterization of the major iron-regulated protein of
Neisseria gonorrhoeae and Neisseria meningitidis.
#accession A60816
#molecule type protein
#residues 23-69 #label MOR
GENETICS
#gene Fbp
#superfamily sfuA protein
CLASSIFICATION iron binding
KEYWORDS
FEATURE 1-22
#domain signal sequence #status experimental #label SIG\
23-330 #product iron-binding protein #status experimental
#label MAT

SUMMARY #length 330 #molecular-weight 35769 #checksum 1901
Query Match 53.8%; Score 50; DB 6; Length 330;
Best Local Similarity 50.0%; Pred. No. 2.08e+01;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 235 Infvhrdpg 244
|||
Qy 1 INFTRQRP 10

Search completed: Thu Apr 3 11:57:09 1997
Job time : 11 secs.

MPSRLH (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Apr 3 11:56:31 1997; MasPar time 1.88 Seconds
137.734 Million cell updates/sec

Tabular output not generated.

Title: >US-08-190-411A-2
Description: (1-14) from 5541104.pep
Perfect Score: 93
Sequence: 1 INFTQRQPSGSS 14

Scoring table: PAM 150
Gap 15

Searched: 52205 seqs, 18531385 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot33
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10

Statistics: Mean 25.1117; Variance 28.639; scale 0.877

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description	Pred. No.
1	93	100.0	309	5	MAG1	HUMAN	MELANOMA-ASSOCIATED A	7.44e-11
2	58	62.4	172	7	RL10	BRUAB	50S RIBOSOMAL PROTEIN	9.69e-02
3	57	61.3	317	5	MAG4	HUMAN	MELANOMA-ASSOCIATED A	1.63e-01
4	57	61.3	651	1	BGLR	HUMAN	BETA-GLUCURONIDASE PR	1.63e-01
5	56	60.2	648	1	BGLR	MOUSE	BETA-GLUCURONIDASE PR	2.74e-01
6	55	59.1	96	9	VPR	HV122	VPR PROTEIN (R ORF PR	4.56e-01
7	55	59.1	96	9	VPR	HV1MA	VPR PROTEIN (R ORF PR	4.56e-01
8	55	59.1	1703	8	SNF2	YEAST	NUCLEAR PROTEIN SNF2	4.56e-01
9	54	58.1	355	10	YNOP	YEAST	HYPOTHETICAL 40.7 KD	7.55e-01
10	53	57.0	96	9	VPR	HV1RH	VPR PROTEIN (R ORF PR	1.24e+00

11	53	57.0	96	9	VPR	HV10Y	VPR PROTEIN (R ORF PR	1.24e+00
12	53	57.0	96	9	VPR	HV1JR	VPR PROTEIN (R ORF PR	1.24e+00
13	53	57.0	638	9	TOXA	PSEAE	EXOTOXIN A PRECURSOR	1.24e+00
14	51	54.8	331	10	YP2E	CAEEL	HYPOTHETICAL 38.3 KD	3.29e+00
15	50	53.8	96	9	VPR	HV1EL	VPR PROTEIN (R ORF PR	5.30e+00
16	50	53.8	330	3	FBP	NEIGO	MAJOR FERRIC IRON BIN	5.30e+00
17	50	53.8	330	3	FBP	NEIME	MAJOR FERRIC IRON BIN	5.30e+00
18	50	53.8	793	2	CLPA	RHOBL	CLPA HOMOLOG PROTEIN	5.30e+00
19	50	53.8	889	9	TRK2	YEAST	POTASSIUM TRANSPORT P	5.30e+00
20	49	52.7	96	9	VPR	HV1N5	VPR PROTEIN (R ORF PR	8.46e+00
21	49	52.7	128	8	RNP	HYDHY	RIBONUCLEASE PANCREAT	8.46e+00
22	49	52.7	155	8	RS7	MYCSM	30S RIBOSOMAL PROTEIN	8.46e+00
23	49	52.7	314	5	MAG2	HUMAN	MELANOMA-ASSOCIATED A	8.46e+00
24	49	52.7	349	6	NRLB	KLEPN	NITRILASE, BROMOXYNIL	8.46e+00
25	49	52.7	494	8	SCRB	STAXY	SUCROSE-6-PHOSPHATE H	8.46e+00
26	49	52.7	542	5	MET7	NEUCR	CYSTATHIONINE GAMMA-S	8.46e+00
27	49	52.7	648	1	BGLR	RAT	BETA-GLUCURONIDASE PR	8.46e+00
28	49	52.7	733	3	ERG7	RAT	LANOSTEROL SYNTHASE (8.46e+00
29	48	51.6	94	8	RT19	PETHY	MITOCHONDRIAL RIBOSOM	1.34e+01
30	48	51.6	96	9	VPR	HV1MN	VPR PROTEIN (R ORF PR	1.34e+01
31	48	51.6	220	9	US02	HSVBS	PROTEIN US2 HOMOLOG	1.34e+01
32	48	51.6	272	5	MCBC	ECOLI	MICROCIN B17 PROCESSI	1.34e+01
33	48	51.6	518	10	YNV6	CAEEL	HYPOTHETICAL 59.0 KD	1.34e+01
34	48	51.6	552	4	HMEN	DROME	SEGMENTATION POLARITY	1.34e+01
35	48	51.6	584	4	HMEN	DROVI	SEGMENTATION POLARITY	1.34e+01
36	48	51.6	3567	3	ERY2	SACER	ERYTHRONOLIDE SYNTHAS	1.34e+01
37	47	50.5	231	9	UCR1	NEUCR	UBIQUINOL-CYTOCHROME	2.11e+01
38	47	50.5	292	4	GTAB	BACSU	UTP--GLUCOSE-1-PHOSPH	2.11e+01
39	47	50.5	305	10	YB3	XENLA	B BOX BINDING PROTEIN	2.11e+01
40	47	50.5	322	2	CBFX	MOUSE	CCAT-BINDING TRANSCR	2.11e+01
41	47	50.5	322	10	YBI	MOUSE	Y BOX BINDING PROTEIN	2.11e+01
42	47	50.5	324	2	CBFX	HUMAN	CCAT-BINDING TRANSCR	2.11e+01
43	47	50.5	631	8	TEC	HUMAN	TYROSINE-PROTEIN KINA	2.11e+01
44	47	50.5	827	7	PLSB	ECOLI	GLYCEROL-3-PHOSPHATE	2.11e+01
45	47	50.5	1060	9	UAY	EMENI	POSITIVE REGULATOR OF	2.11e+01

ALIGNMENTS

RESULT	1	MAG1	HUMAN	STANDARD;	PRT;	309	AA.
ID	P43355;						
AC	01-NOV-1995	(REL. 32, CREATED)					
DT	01-NOV-1995	(REL. 32, LAST SEQUENCE UPDATE)					
DT	01-FEB-1996	(REL. 33, LAST ANNOTATION UPDATE)					
DE	MELANOMA-ASSOCIATED ANTIGEN 1 (MAGE-1 ANTIGEN) (ANTIGEN MZ2-E).						
GN	MAGE1.						
OS	HOMO SAPIENS (HUMAN).						
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;						
OC	EUTHERIA; PRIMATES.						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RX	MEDLINE; 92086861.						
RA	VAN DER BRUGEN P., TRAVERSARI C., CHOMEZ P., LURQUIN C., DE PLAEN E.,						
RA	VAN DEN EYDE B., KNUTH A., BOON T.;						
RL	SCIENCE 254:1643-1647(1991).						
RN	[2]						
RP	SEQUENCE FROM N.A.						
RP	TISSUE=SKIN;						
RC	MEDLINE; 94311935.						
RX							

RA DING M., BECK R.J., KELLER C.J., FENTON R.G.;
RL BIOCHEM. BIOPHYS. RES. COMMUN. 202:549-555(1994).
RN [3]
RP MUTAGENESIS.
RC TISSUE=BLOOD;
RX MEDLINE; 94157413.
RA GAUGLER B., VAN DEN EYNDE B., VAN DER BRUGGEN P., ROMERO P.,
RA GAFORIO J.J., DE PLAEN E., LETHE B., BRASSEUR F., BOON T.;
RL J. EXP. MED. 179:921-930(1994).
CC -1- FUNCTION: NOT KNOWN, THOUGH MAY PLAY A ROLE IN EMBRYONAL
CC DEVELOPMENT AND TUMOR TRANSFORMATION OR ASPECTS OF TUMOR
CC PROGRESSION. ANTIGEN RECOGNIZED ON A MELANOMA BY AUTOLOGOUS
CC CYTOLYTIC T LYMPHOCYTES.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES,
CC SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LUNG
CC CARCINOMA AND BREAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT
CC FOR TESTES. NEVER EXPRESSED IN KIDNEY TUMORS, LEUKEMIAS AND
CC LYMPHOMAS.
CC -1- POLYMORPHISM: THE VARIANT AT POSITION 32 LIKELY REPRESENTS A
CC POLYMORPHISM OF THE MAG-1 GENE.
CC -1- SIMILARITY: BELONGS TO THE MAGE FAMILY.
DR EMBL; M77481; G416115; -.
DR MIM; 600186; 11TH EDITION.
KW ANTIGEN; MULTIGENE FAMILY; POLYMORPHISM; TUMOR ANTIGEN.
FT VARIANT 32 32 T -> A.
FT DOMAIN 33 36 POLY-SER.
FT MUTAGEN 163 163 D->A: ABOLISHES HLA-A1 BINDING.
FT MUTAGEN 169 169 Y->A: ABOLISHES HLA-A1 BINDING.
SQ SEQUENCE 309 AA; 34342 MW; E6CB1300 CRC32;

Query Match 100.0%; Score 93; DB 5; Length 309;
Best Local Similarity 100.0%; Pred. No. 7.44e-11;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 68 inftrgrpseqs 81
Qy 1 INTRORQPSGSS 14
|||||

RESULT 2
ID RL10 BRUAB STANDARD; PRT; 172 AA.
AC P41107;
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE 50S RIBOSOMAL PROTEIN L10.
GN RPLJ
OS BRUCELLA ABORTUS.
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
RN UNCERTAIN.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=19;
RX MEDLINE; 94171071.
RA OLIVEIRA S.C., ZHU Y., SPLITTER G.A.;
RL GENE 140:137-138(1994).
CC -1- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
DR EMBL; L23505; G387911; -.
DR PROSITE; PS01109; RIBOSOMAL_L10.
KW RIBOSOMAL PROTEIN.

SQ SEQUENCE 172 AA; 18459 MW; 196B1070 CRC32;
Query Match 62.4%; Score 58; DB 7; Length 172;
Best Local Similarity 60.0%; Pred. No. 9.69e-02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 13 vkfvtrqcpq 22
Qy 1 INTRORQPS 10
:::|||||

RESULT 3
ID MAG4 HUMAN STANDARD; PRT; 317 AA.
AC P43358;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE MELANOMA-ASSOCIATED ANTIGEN 4 (MAGE-4 ANTIGEN) (MAGE-X2).
GN MAGE4.

OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BLOOD;
RX MEDLINE; 95012457.
RA DE PLAEN E., ARDEN K., TRAVERSARI C., GAFORIO J.J., SZIKORA J.-P.,
RA DE SMET C., BRASSEUR F., VAN DER BRUGGEN P., LETHE B., LORQUIN C.,
RA BRASSEUR R., CHOMEZ P., DE BACKER O., CAVEENE W., BOON T.;
RL IMMUNOGENETICS 40:360-369(1994).
RN [2]
RP SEQUENCE FROM N.A.

RC TISSUE=SKIN;
RX MEDLINE; 94311935.
RA DING M., BECK R.J., KELLER C.J., FENTON R.G.;
RL BIOCHEM. BIOPHYS. RES. COMMUN. 202:549-555(1994).
CC -1- FUNCTION: NOT KNOWN, THOUGH MAY PLAY A ROLE IN EMBRYONAL
CC DEVELOPMENT AND TUMOR TRANSFORMATION OR ASPECTS OF TUMOR
CC PROGRESSION.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES,
CC SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LUNG
CC CARCINOMA AND BREAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT
CC FOR TESTES AND PLACENTA.
CC -1- SIMILARITY: BELONGS TO THE MAGE FAMILY. STRONG SIMILARITY WITH
CC MAGE-1.
DR EMBL; U10687; G533515; -.
DR EMBL; U10688; G533517; -.
DR EMBL; U10340; G499124; -.
KW ANTIGEN; MULTIGENE FAMILY; POLYMORPHISM; TUMOR ANTIGEN.
FT DOMAIN 41 44 POLY-SER.
FT VARIANT 173 173 T -> A.
FT CONFLICT 307 307 E -> Q (IN REF. 2).
SQ SEQUENCE 317 AA; 34929 MW; 3CE38AF9 CRC32;

Query Match 61.3%; Score 57; DB 5; Length 317;
Best Local Similarity 71.4%; Pred. No. 1.63e-01;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 76 isftcwrpseqs 89
:::|||||

QY 1 INFTRQPSSEGS 14

RESULT 4

ID BGLR HUMAN STANDARD; PRT; 651 AA.

AC P08236;

DT 01-AUG-1988 (REL. 08, CREATED)

DT 01-AUG-1988 (REL. 08, LAST SEQUENCE UPDATE)

DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)

DE BETA-GLUCURONIDASE PRECURSOR (EC 3.2.1.31) (BETA-G1).

GN GUSB.

OS HOMO SAPIENS (HUMAN).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; PRIMATES.

[1]

RN SEQUENCE FROM N.A.

RP MEDLINE; 87119233.

RA OSHIMA A., KYLE J.W., MILLER R.D., HOFFMANN J.W., POWELL P.P.,

RA GRUBB J.H., SLY W.S., TROPACK M., GUISE K.S., GRAVEL R.A.;

RL PROC. NATL. ACAD. SCI. U.S.A. 84:685-689 (1987).

[2]

RN SEQUENCE OF 1-70 FROM N.A.

RP MEDLINE; 92009900.

RA SHIPLEY J.M., MILLER R.D., WU B.M., GRUBB J.H., CHRISTENSEN S.G.,

RA KYLE J.W., SLY W.S.;

RA GENOMICS 10:1009-1018 (1991).

[3]

RN SEQUENCE OF 23-32 AND 160-175.

RP TISSUE=PLACENTA;

RC MEDLINE; 92162201.

RA TANAKA J., GASA S., SAKURADA K., MIYAZAKI T., KASAI M., MAKITA A.;

RA BIOL. CHEM. HOPPE-SEYLER 373:57-62 (1992).

[4]

RN VARIANT MPS-VII TRP-216.

RP MEDLINE; 94154730.

RA VERVOORT R., LISSENS W., LIEBAERS I.;

RL HUM. MUTAT. 2:443-445 (1993).

[5]

RN VARIANTS MPS-VII VAL-354 AND TRP-611.

RP MEDLINE; 94154731.

RA WU B.M., SLY W.S.;

RL HUM. MUTAT. 2:446-457 (1993).

[6]

RN VARIANTS MPS-VII CYS-382 AND VAL-619.

RP MEDLINE; 91090114.

RA TOMATSU S., FUKUDA S., SUKEGAWA K., IKEDO Y., YAMADA S., YAMADA Y.,

RA SASAKI T., OKAMOTO H., KUNAHARA T., YAMAGUCHI S., KIMAN T.,

RA SHINTAKO H., ISHIKI G., ORII T.;

RL AM. J. HUM. GENET. 48:89-96 (1991).

[7]

RN VARIANT MPS-VII CYS-627.

RP MEDLINE; 93190983.

RA SHIPLEY J.M., KLINKENBERG M., WU B.M., BACHINSKY D.R., GRUBB J.H.,

RA SLY W.S.;

RL AM. J. HUM. GENET. 52:517-526 (1993).

CC -1- FUNCTION: BETA-GLUCURONIDASE PLAYS AN IMPORTANT ROLE IN THE

CC DEGRADATION OF DERMATAN AND KERATAN SULFATES.

CC -1- CATALYTIC ACTIVITY: A BETA-D-GLUCURONOSIDE + H(2)O = AN

CC ALCOHOL + D-GLUCURONATE.

CC -1- SUBUNIT: HOMOTETRAMER.

-1- SUBCELLULAR LOCATION: LYSOSOMAL.

CC -1- PTM: GLYCOSYLATED WITH 3 TO 4 N-LINKED OLIGOSACCHARIDE CHAINS.

CC -1- DISEASE: DEFECTS IN GUSB ARE THE CAUSE OF MUCOPOLYSACCHARIDOSIS

CC TYPE VII (MPS-VII) (ALSO KNOWN AS SLY SYNDROME).

CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF GLYCOSYL HYDROLASES.

DR EMBL; M15182; G183233; -.

DR EMBL; M63002; G183707; -.

DR PIR; A26581; A26581.

DR MIM; 253220; 11TH EDITION.

DR PROSITE; PS00608; GLYCOSYL HYDROL F2 2.

DR PROSITE; PS00719; GLYCOSYL HYDROL F2 1.

KW HYDROLASE; GLYCOSIDASE; LYSOSOME; GLYCOPROTEIN; SIGNAL;

KW MUCOPOLYSACCHARIDOSIS; DISEASE MUTATION.

FT SIGNAL 1 22

FT CHAIN 23 651 BETA-GLUCURONIDASE.

FT ACT SITE 451 451 PROTON DONOR (BY SIMILARITY).

FT CARBOHYD 173 173

FT CARBOHYD 272 272

FT CARBOHYD 420 420

FT CARBOHYD 631 631

FT CARBOHYD 216 216

FT VARIANT 354 354

FT VARIANT 382 382

FT VARIANT 611 611

FT VARIANT 619 619

FT VARIANT 627 627

FT SEQUENCE 651 AA; 74715 MW; F0E4C8D6 CRC32;

Query Match 61.3%; Score 57; DB 1; Length 651;

Best Local Similarity 63.6%; Pred. No. 1.63e-01;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

DQ 609 ftrgrqpkksaa 619

QY 3 FTRQPSSEGS 13

RESULT 5

ID BGLR MOUSE STANDARD; PRT; 648 AA.

AC P12265;

DT 01-OCT-1989 (REL. 12, CREATED)

DT 01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)

DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)

DE BETA-GLUCURONIDASE PRECURSOR (EC 3.2.1.31).

GN GUS.

OS MUS MUSCULUS (MOUSE).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; RODENTIA.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 88085188.

RA GALLAGHER P.M., D'AMORE M.A., LUND S.D., ELLIOTT R.W., PAZIK J.,

RA HAHMAN C., KORFHAGEN T.R., GANSCHOW R.E.;

RL GENOMICS 1:145-152 (1987).

[2]

RN SEQUENCE FROM N.A.

RP MEDLINE; 9284700.

RA GALLAGHER P.M., D'AMORE M.A., LUND S.D., GANSCHOW R.E.;

RL GENOMICS 2:215-219 (1988).

[3]

RP SEQUENCE FROM N.A.
RX MEDLINE: 89062453.
RA D'AMORE M.A., GALLAGHER P.M., KORFAGEN T.R., GANSCHOW R.E.;
RL BIOCHEMISTRY 27:7131-7140(1988).
RN [4]
RW SEQUENCE FROM N.A.
RX MEDLINE: 89384641.
RA WAWRZYNIAK C.J., GALLAGHER P.M., D'AMORE M.A., CARTER J.E.,
RL LUND S.D., RINCHIK E.M., GANSCHOW R.E.;
RM MOL. CELL. BIOL. 9:4074-4078(1989).
CC -1- FUNCTION: BETA-GLUCURONIDASE PLAYS AN IMPORTANT ROLE IN THE
CC DEGRADATION OF DERMATAN AND KERATAN SULFATES.
CC -1- CATALYTIC ACTIVITY: A BETA-D-GLUCURONOSIDE + H(2)O = AN
CC ALCOHOL + D-GLUCURONATE.
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- SUBCELLULAR LOCATION: LYSOSOMAL.
CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF GLYCOSYL HYDROLASES.
DR EMBL: J03047; G309256; -.
DR EMBL: J02836; G387180; -.
DR EMBL: M63836; G193723; -.
DR PIR: A28954; A28954.
DR PIR: A29977; A29977.
DR PROSITE: P500608; GLYCOSYL HYDROL F2 2.
DR PROSITE: P500719; GLYCOSYL HYDROL F2 1.
DR HYDROLASE; GLYCOSIDASE; LYSOSOME; GLYCOPROTEIN; SIGNAL.
KW SIGNAL 1 22
FT CHAIN 23 648 BETA-GLUCURONIDASE.
FT ACT SITE 447 447 PROTON DONOR (BY SIMILARITY).
FT CARBOHYD 172 172 POTENTIAL.
FT CARBOHYD 416 416 POTENTIAL.
FT CARBOHYD 591 591 POTENTIAL.
FT CARBOHYD 627 627 POTENTIAL.
FT CONFLICT 320 320 V -> I (IN REF. 4).
SQ SEQUENCE 648 AA; 74239 MW; 13A10D2B CRC32;

Query Match 60.2%; Score 56; DB 1; Length 648;
Best Local Similarity 100.0%; Pred. No. 2.74e-01; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

Db 605 ftqrqp 611
| | | | |
Qy 3 FTQRQP 9

RESULT 6
ID VPR HV122 STANDARD; PRT; 96 AA.
AC P12519;
DT 01-OCT-1989 (REL. 12, CREATED)
DT 01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
DT 01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DE VPR PROTEIN (R ORF PROTEIN).
GN VPR.
OS HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z2/CDC-234 ISOLATE) (HIV-1).
OC VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
OC LENTIVIRINAE.
RN [1]
RP SEQUENCE FROM N.A.
RA THEODORE T., BUCKLER-WHITE A.;
RL SUBMITTED (NOV-1988) TO THE HIV DATA BANK.
DR EMBL: M22639; G329383; -.

DR HIV; M22639; VPR\$2226.
KW AIDS.
SQ SEQUENCE 96 AA; 11380 MW; B28C76BE CRC32;
Query Match 59.1%; Score 55; DB 9; Length 96;
Best Local Similarity 57.1%; Pred. No. 4.56e-01; Indels 0; Gaps 0;
Matches 8; Conservative 4; Mismatches 2;

Db 81 igitqrqrarngss 94
| : | | | | : : | | |
Qy 1 INFTRQRPSEGSS 14

RESULT 7
ID VPR HV1MA STANDARD; PRT; 96 AA.
AC P03955;
DT 01-NOV-1988 (REL. 09, CREATED)
DT 01-NOV-1988 (REL. 09, LAST SEQUENCE UPDATE)
DT 01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DE VPR PROTEIN (R ORF PROTEIN).
GN VPR.
OS HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (MAL ISOLATE) (HIV-1).
OC VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
OC LENTIVIRINAE.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 86245056.
RA ALIZON M., WAIN-HOBSON S., MONTAGNIER L., SONIGO P.;
RL CELL 46:63-74(1986).
DR EMBL: K03456; G328024; -.
DR EMBL: X04415; G60232; -.
DR EMBL: A07116; G492875; -.
DR EMBL: K03456; VPR\$MAL.
KW AIDS.
SQ SEQUENCE 96 AA; 11343 MW; 4AA5A84E CRC32;

Query Match 59.1%; Score 55; DB 9; Length 96;
Best Local Similarity 57.1%; Pred. No. 4.56e-01; Indels 0; Gaps 0;
Matches 8; Conservative 4; Mismatches 2;

Db 81 igitqrqrarngss 94
| : | | | | : : | | |
Qy 1 INFTRQRPSEGSS 14

RESULT 8
ID SNF2 YEAST STANDARD; PRT; 1703 AA.
AC P22082;
DT 01-AUG-1991 (REL. 19, CREATED)
DT 01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE NUCLEAR PROTEIN SNF2 (REGULATORY PROTEIN GAMI).
GN SNF2 OR SWI2 OR GAMI OR TYE3 OR RIC1.
OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE: 91187857.
RA LAURENT B.C., TREITEL M.A., CARLSON M.;

RL PROC. NATL. ACAD. SCI. U.S.A. 88:2687-2691 (1991).

RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AH22;
 RX MEDLINE; 91360076.
 RA YOSHIMOTO H., YAMASHITA I.;
 RL MOL. GEN. GENET. 228:270-280 (1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=X2180-1B;
 RX MEDLINE; 95332261.
 RA KODAKI T., HOSAKA K., NIKAWA J., YAMASHITA S.;
 RL J. BIOCHEM. 117:362-368 (1995).
 CC -1- FUNCTION: INVOLVED IN TRANSCRIPTIONAL ACTIVATION, TOGETHER WITH
 CC SNF5, SNF6, SWI3 AND ADR6/SWI1 PROTEINS. SWI PRODUCTS MAY
 CC ASSIST THE FUNCTION OF GENE-SPECIFIC, DEDICATED ACTIVATORS LIKE
 CC ADRL, INO2/INO4, GAL4 AND SWI5.
 CC -1- FUNCTION: REQUIRED FOR TRANSCRIPTION OF SUCROSE FERMENTATION
 CC GENES.
 CC -1- SUBUNIT: ADR6/SWI1, SNF2/SWI2, SWI3, SNF5, AND SNF6 MAY FORM A
 CC VERY LARGE MULTI-SUBUNIT COMPLEX.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- SIMILARITY: STRONG, TO DROSOPHILA BRAHMA.
 CC -1- SIMILARITY: CONTAINS A COPY OF THE BROMODOMAIN.
 CC -1- SIMILARITY: TO HELICASES OF THE SNF2/RAD54 FAMILY.
 DR EMBL; M61703; G172632; -.
 DR EMBL; X57837; G4500; -.
 DR EMBL; D90459; G806532; -.
 DR PIR; S15047; S15047.
 DR PIR; S16820; S16820.
 DR LISTA; SC01149; SNF2.
 DR SGB; L0001945; SNF2.
 DR PROSITE; PS00633; BROMODOMAIN 1.
 DR PROSITE; PS00014; BROMODOMAIN 2.
 KW TRANSCRIPTION REGULATION; NUCLEAR PROTEIN; ACTIVATOR; REPEAT;
 KW BROMODOMAIN; ATP-BINDING; HELICASE.
 FT DOMAIN 55 68 GLN-RICH
 FT DOMAIN 207 239 ALA/GLN-RICH.
 FT NP BIND 792 799 ATP (BY SIMILARITY).
 FT SITE 894 897 DEGH BOX.
 FT DOMAIN 1446 1458 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT DOMAIN 1505 1522 9 X 2 AA TANDEM REPEATS OF R-G.
 FT DOMAIN 1568 1638 BROMODOMAIN.
 SQ SEQUENCE 1703 AA; 194050 MW; CA278760 CRC32;

Query Match 59.1%; Score 55; DB 8; Length 1703;
 Best Local Similarity 50.0%; Pred. No. 4.56e-01;
 Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 299 efarrqptd 308
 QY 2 NFTTRQPFSE 11
 :|:|:|:|:|:|

RESULT 9
 ID YNOP YEAST STANDARD; PRT; 355 AA.
 AC P48559;
 DT 01-FEB-1996 (REL. 33, CREATED)
 DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)

DE HYPOTHETICAL 40.7 KD GTP-BINDING PROTEIN IN MCK1-RP55B INTERGENIC
 DE REGION.
 GN NO410.
 OS SAGCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FY1679;
 RX MEDLINE; 96132033.
 RA MAURER K.C.T., URBANUS J.H.M., PLANTA R.J.;
 RL YEAST 11:1303-1310 (1995).
 DR EMBL; U23084; G1050856; -.
 KW HYPOTHETICAL PROTEIN; GTP-BINDING; LIPOPROTEIN; PRENYLATION.
 FT NP BIND 35 42 GTP (POTENTIAL).
 FT NP BIND 166 170 GTP (POTENTIAL).
 FT NP BIND 230 233 GTP (POTENTIAL).
 FT LIPID 353 353 GERANYL-GERANYL (BY SIMILARITY).
 FT LIPID 354 354 GERANYL-GERANYL (BY SIMILARITY).
 SQ SEQUENCE 355 AA; 40678 MW; 9E3B3359 CRC32;

Query Match 58.1%; Score 54; DB 10; Length 355;
 Best Local Similarity 87.5%; Pred. No. 7.55e-01;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 321 fnftrqrq 328
 QY 1 INFTRQRQ 8
 :|:|:|:|:|:|

RESULT 10
 ID VPR HVIRH STANDARD; PRT; 96 AA.
 AC P05954;
 DT 01-NOV-1988 (REL. 09, CREATED)
 DT 01-NOV-1988 (REL. 09, LAST SEQUENCE UPDATE)
 DT 01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
 DE VPR PROTEIN (R ORF PROTEIN).
 GN VPR.
 OS HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (RF/HAT ISOLATE) (HIV-1).
 OC VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
 OC LENTIVIRINAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STARCICH B.R., HAHN B.H., SHAW G.M., MCNEELY P.D., MODROW S.,
 RA WOLF H., PARKS E.S., PARKS W.P., JOSEPHS S.F., GALLO R.C.,
 RA WONG-STAL F.;
 RL SUBMITTED (XXX-1987) TO THE HIV DATA BANK.
 DR EMBL; M17451; G328571; -.
 DR HIV; M17451; VPRSRF.
 KW AIDS.

Query Match 57.0%; Score 53; DB 9; Length 96;
 Best Local Similarity 50.0%; Pred. No. 1.24e+00;
 Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 81 igitqrarqas 94
 QY 1 INFTRQRQSEGSS 14
 :|:|:|:|:|:|

RESULT 11
ID VPR HV10Y STANDARD; PRT; 96 AA.
AC P20891;
DT 01-FEB-1991 (REL. 17, CREATED)
DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
DT 01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DE VPR PROTEIN (R ORF PROTEIN).
GN VPR.
OS HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (OYI ISOLATE) (HIV-1).
OC VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
OC LENTIVIRINAE.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90148544.
RA HUET T., DAZZA M.C., BRUN-VEZINET F., ROELANTS G.E., WAIN-HOBSON S.;
RL AIDS 3:707-715(1989).
CC -|- THE OYI ISOLATE WAS TAKEN FROM THE BLOOD OF A HEALTHY GABONESE
CC INDIVIDUAL.
DR EMBL; M26727; G328446; --.
DR HIV; M26727; VPR\$OYI.
KW AIDS.
SQ SEQUENCE 96 AA; 11494 MW; 4C01E21D CRC32;
Query Match 57.0%; Score 53; DB 9; Length 96;
Best Local Similarity 50.0%; Pred. No. 1.24e+00;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
Db 81 igitrqrarngas 94
|:||||: |:|
QY 1 INFTQRQPSGSS 14

RESULT 12
ID VPR HV1JR STANDARD; PRT; 96 AA.
AC P20883;
DT 01-FEB-1991 (REL. 17, CREATED)
DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
DT 01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DE VPR PROTEIN (R ORF PROTEIN).
GN VPR.
OS HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (JRCFS ISOLATE) (HIV-1).
OC VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
OC LENTIVIRINAE.
RN [1]
RP SEQUENCE FROM N.A.
RA KOYANAGI S., CHEN I.S.Y.;
RL SUBMITTED (DEC-1988) TO THE HIV DATA BANK.
DR EMBL; M38429; G327817; --.
DR HIV; M38429; VPR\$JRCFS.
KW AIDS.
SQ SEQUENCE 96 AA; 11419 MW; 1DC76121 CRC32;
Query Match 57.0%; Score 53; DB 9; Length 96;
Best Local Similarity 50.0%; Pred. No. 1.24e+00;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
Db 81 igitrqrarngas 94
|:||||: |:|
QY 1 INFTQRQPSGSS 14

RESULT 13
ID TOXA PSEAE STANDARD; PRT; 638 AA.
AC P11439;
DT 01-OCT-1989 (REL. 12, CREATED)
DT 01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE EXOTOXIN A PRECURSOR (NAD-DEPENDENT ADP-RIBOSYLTRANSFERASE
DE (EC 2.4.2.-)).
GN ETA.
OS PSEUDOMONAS AERUGINOSA.
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
OC PSEUDOMONADACEAE.
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 26-53.
RX MEDLINE; 84194063.
RA GRAY G.L., SMITH D.H., BALDRIDGE J.S., HARKINS R.N., VASIL M.L.,
RA CHEN E.Y., HEYNEKER H.L.;
RL PROC. NATL. ACAD. SCI. U.S.A. 81:2645-2649(1984).
RN [2]
RP ACTIVE SITE.
RX MEDLINE; 87250491.
RA CARROLL S.F., COLLIER R.J.;
RL J. BIOL. CHEM. 262:8707-8711(1987).
RN [3]
RP DOMAINS.
RX MEDLINE; 90375493.
RA CHAUDHARY V.K., JINNO Y., GALO M.G., FITZGERALD D., PASTAN I.;
RL J. BIOL. CHEM. 265:16306-16310(1990).
RN [4]
RP DOMAINS.
RX MEDLINE; 91006124.
RA BOURDET S., VACHERON M.-J., GUINAND M., MICHEL G., ARMINJON F.;
RL EUR. J. BIOCHEM. 192:379-385(1990).
CC -|- FUNCTION: THIS TOXIN IS AN NAD-DEPENDENT ADP-RIBOSYLTRANSFERASE.
CC IT CATALYZES THE TRANSFER OF THE ADP RIBOSYL MOIETY OF OXIDIZED
CC NAD ONTO ELONGATION FACTOR 2 (EF-2) THUS ARRESTING PROTEIN
CC SYNTHESIS.
CC -|- PTM: THE 8 CYSTEINES PARTICIPATE IN INTRACHAIN DISULFIDE BONDS.
CC -|- SIMILARITY: REGIONAL SEQUENCE SIMILARITY AT THE ACTIVE SITE
CC WITH DIPHTHERIA TOXIN (DT).
DR EMBL; K01397; G151216; --.
DR PIR; A30347; A30347.
KW TOXIN; SIGNAL; ADP-RIBOSYLATION; TRANSFERASE; GLYCOSYLTRANSFERASE;
KW NAD.
FT SIGNAL 1 25
FT CHAIN 26 638
FT DOMAIN 26 277
FT DOMAIN 278 389
FT DOMAIN 390 429
FT DOMAIN 430 638
FT ACT SITE 491 491
FT ACT SITE 578 578
FT ACT SITE 638 AA; 69309 MW; 33D9876A CRC32;
SQ SEQUENCE 638 AA; 69309 MW; 33D9876A CRC32;
Query Match 57.0%; Score 53; DB 9; Length 638;
Best Local Similarity 85.7%; Pred. No. 1.24e+00;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 297 ftrhrqp 303
|:|:|:|:|
Qy 3 FTRORQP 9

RESULT 14
ID YP2E CAEL STANDARD; PRT; 331 AA.
AC Q09212; 1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 38.3 KD PROTEIN AH6.14 IN CHROMOSOME II.
GN AH6.14.
OS CAENORHABDITIS ELEGANS.
OC EUKARYOTA; METAZOA; ACCELLOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA JASSAL B.;
RL SUBMITTED (JAN-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -!- SIMILARITY: BELONGS TO A FAMILY THAT CURRENTLY CONSISTS OF AH6.4,
CC AH6.6, AH6.7, AH6.8, AH6.9, AH6.10, AH6.11, AH6.12 AND AH6.14.
DR EMBL; Z48009; G643104; -.
DR WORPEP; AH6.14; CE01455.
KW HYPOTHETICAL PROTEIN; TRANSMEMBRANE.
FT TRANSMEM 26 46 POTENTIAL.
FT TRANSMEM 104 124 POTENTIAL.
FT TRANSMEM 143 163 POTENTIAL.
FT TRANSMEM 189 209 POTENTIAL.
FT TRANSMEM 238 258 POTENTIAL.
FT TRANSMEM 275 295 POTENTIAL.
SQ SEQUENCE 331 AA; 38284 MW; E9D38381 CRC32;

Query Match 54.8%; Score 51; DB 10; Length 331;
Best Local Similarity 54.5%; Pred. No. 3.29e+00;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 310 leftkqkgsqe 320
|:|:|:|:|
Qy 1 INFTRORPSE 11

RESULT 15
ID VPR HVIEL STANDARD; PRT; 96 AA.
AC P05956;
DT 01-NOV-1988 (REL. 09, CREATED)
DT 01-NOV-1988 (REL. 09, LAST SEQUENCE UPDATE)
DT 01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DE VPR PROTEIN (R ORF PROTEIN).
GN VPR.
OS HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (ELI ISOLATE) (HIV-1).
OC VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
OC LENTIVIRINAE.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 86245056.
RA ALIZON M.; WAIN-HOBSON S.; MONTAGNIER L.; SONIGO P.;
RL CELL 46:63-74(1986).

DR EMBL; K03454; G326681; -.
DR EMBL; X04414; G60171; -.
DR EMBL; A07108; G492867; -.
DR HIV; K03454; VPRSELI.
KW AIDS.
SQ SEQUENCE 96 AA; 11306 MW; FE489F84 CRC32;

Query Match 53.8%; Score 50; DB 9; Length 96;
Best Local Similarity 50.0%; Pred. No. 5.30e+00;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
Db 81 igilqrqrangss 94
|:|:|:|:|
Qy 1 INFTRORPSEGS 14

Search completed: Thu Apr 3 11:56:40 1997
Job time : 9 secs.

M P S R L H

(TM)

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MParch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Apr 3 11:58:45 1997; MasPar time 1.75 Seconds
70.440 Million cell updates/sec

Tabular output not generated.

Title: >US-08-190-411A-3
Description: (1-12) from 5541104.pep
Perfect Score: 82
Sequence: 1 LFRVITKKVAD 12

Scoring table: PAM 150
Gap 15

Searched: 88003 seqs, 10295656 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq25
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18

Statistics: Mean 17.690; Variance 48.071; scale 0.368

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description	Pred. No.
1	82	100.0	12	15	R80619	Immunogenic peptide o	4.06e-03
2	82	100.0	309	13	R70909	Human melanoma antige	4.06e-03
3	65	79.3	10	9	R47325	HLA-A3 MAGE 1 antigen	6.22e-01
4	58	70.7	9	13	R65120	MAGE 1 immunogenic pe	4.50e+00
5	58	70.7	9	9	R47324	HLA-A3 MAGE 1 antigen	4.50e+00
6	58	70.7	9	9	R49228	HLA-A11 MAGE 1 antigen	4.50e+00
7	58	70.7	10	13	R65125	MAGE 1 immunogenic pe	4.50e+00
8	58	70.7	10	9	R49230	HLA-A11 MAGE 1 antigen	4.50e+00
9	47	57.3	309	13	R67916	(1-3)-beta-D-glucan s	8.70e+01
10	47	57.3	722	18	R98227	Rat neuronal protein	8.70e+01
11	46	56.1	140	1	P91891	Part of the sequence	1.13e+02
12	46	56.1	330	1	P81996	Sequence encoded by n	1.13e+02
13	46	56.1	728	17	R90617	Sulfolobus solfataric	1.13e+02
14	45	54.9	159	12	R60900	Borrelia VSDA antigen	1.45e+02
15	45	54.9	173	12	R60908	Borrelia PBI antigen	1.45e+02
16	45	54.9	173	12	R62793	Borrelia KLI1 antigen	1.45e+02
17	45	54.9	174	12	R62786	Borrelia VSDA antigen	1.45e+02
18	45	54.9	175	12	R62784	Borrelia M37 antigen	1.45e+02
19	45	54.9	177	12	R62790	Borrelia IP90 antigen	1.45e+02
20	45	54.9	177	12	R62792	Borrelia B1TS antigen	1.45e+02
21	45	54.9	177	12	R60904	Borrelia IP90 antigen	1.45e+02
22	45	54.9	189	12	R60907	Borrelia KLI1 antigen	1.45e+02
23	45	54.9	191	12	R60898	Borrelia M37 antigen	1.45e+02
24	45	54.9	193	12	R60906	Borrelia B1TS antigen	1.45e+02
25	45	54.9	207	17	R75730	B. burgdorferi strain	1.45e+02
26	45	54.9	209	17	R75728	B. burgdorferi strain	1.45e+02
27	45	54.9	277	16	R48747	G-protein coupled odo	1.45e+02
28	45	54.9	312	5	R27875	Odorant receptor clon	1.45e+02
29	45	54.9	434	7	R36724	2,2-dialkylglycine de	1.45e+02
30	45	54.9	434	12	R62042	Dialkylglycine decarb	1.45e+02
31	45	54.9	779	18	R98226	Rat neuronal protein	1.45e+02
32	44	53.7	176	12	R62775	Borrelia 297 antigen	1.87e+02
33	44	53.7	177	12	R62774	Borrelia 297 antigen	1.87e+02
34	44	53.7	192	12	R60889	Borrelia 297 antigen	1.87e+02
35	44	53.7	212	6	R32353	Cyclophilin C.	1.87e+02
36	44	53.7	322	1	P93306	Fungal lipase	1.87e+02
37	43	52.4	188	9	R49580	Sequence of truncated	2.41e+02
38	43	52.4	194	9	R49581	Sequence of endonucle	2.41e+02
39	43	52.4	295	16	R48758	Human cytomegalovirus	2.41e+02
40	43	52.4	304	11	R56480	I-19 B-lymphocyte der	2.41e+02
41	43	52.4	317	11	R60599	Hornet phospholipase	2.41e+02
42	43	52.4	1274	7	R34714	Bacillus subtilis erf	2.41e+02
43	43	52.4	1456	9	R49042	NMDA receptor channel	2.41e+02
44	43	52.4	1482	9	R45944	Glutamic acid recepto	2.41e+02
45	43	52.4	1484	16	R92507	Human NMDA receptor R	2.41e+02

ALIGNMENTS

RESULT 1

R80619 standard; Protein; 12 AA.

AC R80619;

DE 28-FEB-1996 (first entry)

DE Immunogenic peptide of tumour rejection antigen (MAGE-1).

KW Tumour rejection antigen; MAGE-1; monoclonal antibody; MAB;

KW diagnosis; immunoassay; cancer; immunogen; antisera.

OS Homo sapiens.

PN W09520974-A1.

PD 10-AUG-1995.

PF 05-JAN-1995; U00095.

PR 01-FEB-1994; US-190411.

PA (LUDW-) LUDWIG INST CANCER RES.

PA (SLOK) SLOAN KETTERING INST CANCER RES.

PA (SLOK) MEMORIAL SLOAN-KETTERING CANCER CENT.

PI Boon-falleur T, Chen Y, Garin-chesa P, Old LJ, Rettig WJ;

PI Stockert E, Van der bruggen P;

DR WPI; 95-283606/37.

PT New monoclonal antibody binding specifically to MAGE-1 - useful for

PT diagnosis and monitoring of cancer, also new hybridomas, recombinant

PT MAGE-1 and immunogenic peptide(s).

PS Claim 12; Page 20; 33pp; English.

CC A monoclonal antibody directed against the tumour rejection antigen

CC (MAGE-1) can be used to detect MAGE-1 in samples by standard

CC immunoassay methods for diagnosis and monitoring of cancer etc. The

CC monoclonal antibody is designated MA454 and is produced by the

CC hybridoma deposited as ATCC HB11540. The monoclonal antibody is

CC specific for MAGE-1, having no reactivity for MAGE-2 or MAGE-3.

CC Peptide fragments of MAGE-1 (See R80618-20) may be useful as

CC immunogens for production of the monoclonal antibody and antisera.

SQ Sequence 12 AA;

Query Match 100.0%; Score 82; DB 15; Length 12;

Best Local Similarity 100.0%; Pred. No. 4.06e-03; Indels 0; Gaps 0;

Matches 12; Conservative 0; Mismatches 0;

Db 1 lfravittkkvad 12

Qy 1 LFRAVITKKVAD 12

RESULT 2

ID R70909 standard; Protein; 309 AA.

AC R70909;

DE 09-OCT-1995 (first entry)

DE Human melanoma antigen MAGE-1.

KW Human melanoma antigen; MAGE-1; vaccines; MAGE associated tumours;

KW HLA-restricted cytotoxic T-lymphocyte activity.

OS Homo sapiens.

PN W09504542-A.

PD 16-FEB-1995.

PF 02-AUG-1994; U08721.

PR 06-AUG-1993; US-103623.

PA (CVTE-) CVTEL CORP.

PI Fikes JD, Livingston BD, Sette AD, Sidney JC;

DR WPI; 95-090681/12.

DR N-PSDB; 085435.

PT Human melanoma antigen, MAGE-1, peptide(s) - useful for

PT stimulating immune response against melanoma

PS Example 1; Fig 1; 59pp; English.

CC Q85435 encodes R70909 human melanoma antigen MAGE-1, it was used

CC to produce the C-terminal MAGE-1 peptides described in R70915 to
CC R70969. These peptides are useful for defining epitopes that
CC engender a HLA-restricted cytotoxic lymphocyte activity against
CC MAGE-1 antigens. Compsns. containing these peptides can be
CC administered, as a vaccine to patients susceptible to MAGE
CC associated tumours, e.g. melanomas.
SQ Sequence 309 AA;

Query Match 100.0%; Score 82; DB 13; Length 309;
Best Local Similarity 100.0%; Pred. No. 4.06e-03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 97 lfravittkvad 108
Qy 1 LFRAVITTKVAD 12

RESULT 3

ID R47325 standard; Protein; 10 AA.

AC R47325; 1994 (first entry)
DE HLA-A3 MAGE 1 antigen peptide fragment 96-105.
DT Immunogenic; HLA-A3.2; HLA-A1; binding motif; MHC molecule;
KW immune response; viral infection; cancer; prostate cancer; lymphoma;
KW hepatitis; AIDS; antibody; diagnosis; melanoma antigen.
OS Synthetic.
PN W09403205-A.
PD 17-FEB-1994.
PF 06-AUG-1993; U07421.
PR 07-AUG-1992; US-926666.
ER 05-MAR-1993; US-027746.

FA (CYTE-) CYTEL CORP.

PI Celis E, Grey HM, Kubo RT, Sette A;

DR WPI; 94-065403/08.

PT Peptide which specifically binds selected MHC allele - used to

PT induce an immune response for treatment or prevention of viral

PT infection or cancer, or for diagnosis

PS Example 8; Page 52; 150pp; English.

CC The sequences given in R47304-33 and R49201-44 are immunogenic

CC peptides which have a HLA-A3.2, HLA-A1 or a HLA-A11 binding motif.

CC These peptides may be used in the composition of the invention.

CC These peptides are capable of binding selected MHC molecules and

CC inducing an immune response. They can be used to treat and/or

CC prevent viral infection and cancer, eg. prostate cancer, lymphoma,

CC hepatitis or AIDS. They can also be used to produce antibodies for

CC use as diagnostic or therapeutic agents. The peptides can also be

CC used as diagnostic agents.

SQ Sequence 10 AA;

Query Match 79.3%; Score 65; DB 9; Length 10;

Best Local Similarity 100.0%; Pred. No. 6.22e-01;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 lfravittk 10
Qy 1 LFRAVITTK 9

RESULT 4

ID R65120 standard; peptide; 9 AA.

AC R65120;
DT 09-OCT-1995 (first entry)
DE MAGE 1 immunogenic peptide 96-104.
KW MAGE 1; immunogenic peptide 96-104; cytotoxic C cells;
KW in vitro activation; cancer; AIDS; bacterial infections; malaria;
KW fungal infections; tuberculosis; hepatitis.
OS Homo sapiens.
PN W09504817-A.
PD 16-FEB-1995.
PF 01-AUG-1994; U08672.
PR 06-AUG-1993; US-103401.
PA (CYTE-) CYTEL CORP.

PI Celis E, Kubo R, Serra H, Tsai V, Wentworth P;

DR WPI; 95-090895/12.

PT In vitro activation of cytotoxic T cells for selected killing of

PT target cells - for treating e.g. cancer, AIDS, hepatitis etc.by

PT incubating them with antigen presenting cells loaded with

PT appropriate immunogenic peptide

PS Example 3; Page 35; 53pp; English.

CC R65109-R65145 are immunogenic peptides, they are used in a new

CC method for the in vitro activation of cytotoxic T cells (CFC).

CC This is achieved by incubating the CTCs with antigen presenting

CC cells loaded with an appropriate immunogenic peptide (e.g. one

CC of the above peptides). By selecting the peptides used the

CC following diseases and infections can be treated; cancer, AIDS,

CC hepatitis, other viral and bacterial infections, malaria and

CC tuberculosis.

SQ Sequence 9 AA;

Query Match 70.7%; Score 58; DB 13; Length 9;

Best Local Similarity 100.0%; Pred. No. 4.50e+00;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 lfravittk 9
Qy 1 LFRAVITTK 8

RESULT 5

ID R47324 standard; Protein; 9 AA.

AC R47324;

DT 31-AUG-1994 (first entry)

DE HLA-A3 MAGE 1 antigen peptide fragment 96-104.

KW Immunogenic; HLA-A3.2; HLA-A1; binding motif; MHC molecule;

KW immune response; viral infection; cancer; prostate cancer; lymphoma;

KW hepatitis; AIDS; antibody; diagnosis; melanoma antigen.

OS Synthetic.

PN W09403205-A.

PD 17-FEB-1994.

PF 06-AUG-1993; U07421.

PR 07-AUG-1992; US-926666.

PR 05-MAR-1993; US-027746.

PA (CYTE-) CYTEL CORP.

PI Celis E, Grey HM, Kubo RT, Sette A;

DR WPI; 94-065403/08.

PT Peptide which specifically binds selected MHC allele - used to

PT induce an immune response for treatment or prevention of viral

PT infection or cancer, or for diagnosis

PS Example 8; Page 52; 150pp; English.

CC The sequences given in R47304-33 and R49201-44 are immunogenic

CC peptides which have a HLA-A3.2, HLA-A1 or a HLA-A11 binding motif.
CC These peptides may be used in the composition of the invention.
CC These peptides are capable of binding selected MHC molecules and
CC inducing an immune response. They can be used to treat and/or
CC prevent viral infection and cancer, eg. prostate cancer, lymphoma,
CC hepatitis or AIDS. They can also be used to produce antibodies for
CC use as diagnostic or therapeutic agents. The peptides can also be
CC used as diagnostic agents.
SQ Sequence 9 AA;

Query Match 70.7%; Score 58; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.50e+00;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 lfravtk 9
|||||||
QY 1 LFRAVITK 8

RESULT 6
ID R49228 standard; Protein; 9 AA.
AC R49228;
DE 31-AUG-1994 (first entry)
DE HLA-A11 MAGE 1 antigen peptide fragment 1072.13.
KW Immunogenic; HLA-A3.2; HLA-A1; HLA-A11; binding motif; MHC molecule;
KW immune response; viral infection; cancer; prostate cancer; lymphoma;
KW hepatitis; AIDS; antibody; diagnosis; melanoma antigen.
OS Synthetic.
PN WO9403205-A.
PD 17-FEB-1994.
PF 06-AUG-1993; U07421.
PR 07-AUG-1992; US-926666.
PR 05-MAR-1993; US-027746.
PA (CYTE-) CYTEL CORP.
PI Celis E, Grey HM, Kubo RT, Sette A;
DR WPI; 94-065403/08.
PT Peptide which specifically binds selected MHC allele - used to
PT induce an immune response for treatment or prevention of viral
PT infection or cancer, or for diagnosis.
PS Example 16; Page 116; 150pp; English.

CC The sequences given in R47304-33 and R49201-44 are immunogenic
CC peptides which have a HLA-A3.2, HLA-A1 or a HLA-A11 binding motif.
CC These peptides may be used in the composition of the invention.
CC These peptides are capable of binding selected MHC molecules and
CC inducing an immune response. They can be used to treat and/or
CC prevent viral infection and cancer, eg. prostate cancer, lymphoma,
CC hepatitis or AIDS. They can also be used to produce antibodies for
CC use as diagnostic or therapeutic agents. The peptides can also be
CC used as diagnostic agents.
SQ Sequence 9 AA;

Query Match 70.7%; Score 58; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.50e+00;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 lfravtk 9
|||||||
QY 1 LFRAVITK 8

RESULT 7
ID R65125 standard; peptide; 10 AA.

AC R65125;
DT 09-OCT-1995 (first entry)
DE MAGE 1 immunogenic peptide 95-104.
DE MAGE 1; immunogenic peptide 95-104; cytotoxic C cells;
KW in vitro activation; cancer; AIDS; bacterial infections; malaria;
KW fungal infections; tuberculosis; hepatitis.
OS Homo sapiens.

PN WO9504817-A.
PD 16-FEB-1995.
PF 01-AUG-1994; U08672.
PR 06-AUG-1993; US-103401.
PA (CYTE-) CYTEL CORP.

PI Celis E, Kubo R, Serra H, Tsai V, Wentworth P;
DR WPI; 95-090895/12.
PT In vitro activation of cytotoxic T cells for selected killing of
PT target cells - for treating e.g. cancer, AIDS, hepatitis etc.by
PT incubating them with antigen presenting cells loaded with
PT appropriate immunogenic peptide
PS Example 3; Page 35; 53pp; English.

CC R65109-R65145 are immunogenic peptides, they are used in a new
CC method for the in vitro activation of cytotoxic T cells (CTC).
CC This is achieved by incubating the CTCs with antigen presenting
CC cells loaded with an appropriate immunogenic peptide (e.g. one
CC of the above peptides). By selecting the peptides used the
CC following diseases and infections can be treated; cancer, AIDS,
CC hepatitis, other viral and bacterial infections, malaria and
CC tuberculosis.
SQ Sequence 10 AA;

Query Match 70.7%; Score 58; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.50e+00;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 3 lfravtk 10
|||||||
QY 1 LFRAVITK 8

RESULT 8
ID R49230 standard; Protein; 10 AA.

AC R49230;
DT 31-AUG-1994 (first entry)
DE HLA-A11 MAGE 1 antigen peptide fragment 1072.15.
DE Immunogenic; HLA-A3.2; HLA-A1; HLA-A11; binding motif; MHC molecule;
KW immune response; viral infection; cancer; prostate cancer; lymphoma;
KW hepatitis; AIDS; antibody; diagnosis; melanoma antigen.
OS Synthetic.

PN WO9403205-A.
PD 17-FEB-1994.
PF 06-AUG-1993; U07421.
PR 07-AUG-1992; US-926666.
PR 05-MAR-1993; US-027746.

PA (CYTE-) CYTEL CORP.
PI Celis E, Grey HM, Kubo RT, Sette A;
DR WPI; 94-065403/08.

PT Peptide which specifically binds selected MHC allele - used to
PT induce an immune response for treatment or prevention of viral
PT infection or cancer, or for diagnosis

PS Example 16; Page 116; 150pp; English.
 CC The sequences given in R47304-33 and R49201-44 are immunogenic
 CC peptides which have a HLA-A3.2, HLA-A1 or a HLA-A11 binding motif.
 CC These peptides may be used in the composition of the invention.
 CC These peptides are capable of binding selected MHC molecules and
 CC inducing an immune response. They can be used to treat and/or
 CC prevent viral infection and cancer, eg. prostate cancer, lymphoma,
 CC hepatitis or AIDS. They can also be used to produce antibodies for
 CC use as diagnostic or therapeutic agents. The peptides can also be
 CC used as diagnostic agents.
 SQ Sequence 10 AA;
 Query Match 70.7%; Score 58; DB 9; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.50e+00;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 3 lfpravtk 10
 |||||
 QY 1 LFRVITK 8

RESULT 9
 ID R67916 standard; Protein; 309 AA.
 AC R67916;
 DT 14-SEP-1995 (first entry)
 DE (1-3)-beta-D-glucan sensitive factor.
 DE (1-3)-beta-D-glucan sensitive factor; antifungal agent;
 KW mycosis diagnosis.
 KW Limulus sp.
 OS Key
 FH Peptide 1..31
 FT /label= sig.peptide
 FN W09501432-A.
 PD 12-JAN-1995.
 PF 29-JUN-1994; J01057.
 PR 29-JUN-1993; JP-184403.
 PA (SEKK) SEIKAGAKU KOGYO CO LTD.
 FI Iwanaga S, Muta T, Oda T, Seki N;
 DR N-PSDB; Q81335.
 DR DNA encoding a polypeptide comprising a tetrapeptide motif at
 PT least once - which may be used as an antibacterial and
 PT antifungal.
 PS Claim 11; Pages 32-38; 51pp; Japanese.
 CC Q81335 encodes R67916 a (1-3)-beta-D-glucan sensitive factor, it
 CC has a high affinity for the (1-3)-beta-D-glucan found in fungal
 CC cell walls. The protein is therefore useful for clinically
 CC diagnosing mycosis, and as an antifungal agent for the removal
 CC of fungi.
 SQ Sequence 309 AA;
 Query Match 57.3%; Score 47; DB 13; Length 309;
 Best Local Similarity 50.0%; Pred. No. 8.70e+01;
 Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 40 frpvitriig 49
 |||||
 QY 2 FRAVITKVA 11

RESULT 10
 ID R98227 standard; Protein; 722 AA.
 AC R98227;
 DT 23-SEP-1996 (first entry)
 DE Rat neuronal protein kinase MARK-2.
 DE Neuronal protein kinase; NPK; Microtubule associated protein;
 KW MAP; tau protein; phosphorylation; NPK inhibitor; Alzheimer disease;
 KW cancer; therapy; diagnosis.
 OS Rattus norvegicus.
 PN W09613592-A2.
 PD 09-MAY-1996.
 PF 30-OCT-1995; E04258.
 PR 28-OCT-1994; EP-117122.
 PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 PI Biernat J, Drewes G, Mandelkow E;
 DR WPI; 96-251461/25.
 PT DNA encoding neuronal protein kinase (NPK) - useful for identifying
 PT NPK inhibitors for treatment of Alzheimer's disease and cancer.

PS Claim 1; Page 44-45; 77pp; English.
 CC A novel rat neuronal protein kinase (R98227), designated NPK MARK-2,
 CC is capable of phosphorylating a KXGS sequence motif in tau protein
 CC and microtubule associated proteins MAP4, MAP2 and MAP2c (see also
 CC R98229-39 and W00850-54), causing their dissociation from microtubules.
 CC Phosphorylation of human tau Ser-262 is indicative of the onset of
 CC Alzheimer's disease. MARK-1 is the product of a cDNA clone obtd.
 CC from a rat brain cDNA library by screening with probes derived
 CC from pig brain peptide sequences (see also R98240-50). Another NPK,
 CC MARK-1 (R98226), was similarly isolated. Inhibitors (e.g. antibodies)
 CC of NPKs are used to treat Alzheimer's disease and cancer. NPKs are
 CC themselves used for in vitro diagnosis and/or monitoring of
 CC Alzheimer's disease and cancer.
 SQ Sequence 722 AA;

Query Match 57.3%; Score 47; DB 18; Length 722;
 Best Local Similarity 60.0%; Pred. No. 8.70e+01;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Db 97 lfrevrimkv 106
 |||||
 QY 1 LFRVITKKV 10

RESULT 11
 ID P91891 standard; Protein; 140 AA.
 AC P91891;
 DT 29-APR-1990 (first entry)
 DE Part of the sequence of the Brazil nut 2S-albumin as encoded in the
 DE pBN2S1 plasmid
 KW 2S-albumin; brazil nut; pBN2S1; storage protein gene;
 KW heterologous polypeptide.
 OS Brazil nut.
 FH Key Location/Qualifiers
 FT peptide 1..30
 FT /note="signal peptide"
 FT protein 31..38
 FT /note="mature small subunit"
 FT region 39..43
 FT /note="processing site"
 FT protein 44..136
 FT /note="mature large subunit"

PN	W08903887-A.
PD	05-MAY-1989.
PF	20-OCT-1988; E00944.
PF	20-OCT-1987; EP-402348.
PR	(PLAN-) Plant Genetic Syst.
PI	Vandekerckhove JS, Krebbers E, Leemans J;
PI	WPI; 89-150783/20.
DR	N-FSDB; N91699.
DR	Recombinant DNA expression in plants
PT	- using modified storage protein genes for expressing
PT	heterologous polypeptide(s) in the seeds
PT	Figure 4; 121pp; English.
CC	The entire 2S-albumin storage protein precursor including
CC	signal peptide. It is to be inserted into plants under the control of
CC	a seed-specific promoter and expressed at high levels only or mostly
CC	in the seed forming stage and produced mostly in the seeds.
CC	Sequence 140 AA;
SQ	

Query Match	56.1%;	Score 46;	DB 1;	Length 140;
Best Local Similarity	45.5%;	Pred. No. 1.13e+02;		
Matches	5;	Conservative	2;	Mismatches 4; Indels 0; Gaps 0;

Db	17	fratvtttve	27
		: :	
Qv	2	FRAVITKKVAD	12

RESULT	12
ID	P81996 standard; protein; 330 AA.
AC	P81996;
DE	17-DEC-1990 (first entry)
DE	Sequence encoded by nodulation regulatory gene 2 (nodB-2) of
DE	Bradyrhizobium japonicum strain USDA 123
DE	Bradyrhizobium japonicum strain USDA 123
DE	Rhizobium; symbiosis; legume.
KW	Bradyrhizobium japonicum USDA 123.
OS	

17-JUN-1987; U01421.
17-JUN-1986; US-873297.
PR 11-JUN-1987; US-061848.
P (LUBR) Lubrizol Genetics I.
PPI Appelbaum ER, Hennecke H, Lamb JW, Gottfert M;
WPI; 88-014399/02.
DR N-PSDB; N82007.
DR DNA contg. modulation regulatory genes (nod D) -
from Bradyrhizobium japonicum strains, useful for selective
expression of structural genes
PT Disclosure; 4-4; 88pp; English.
PT DNA sequence of the nodD-1 gene, coding region of B. japonicum USDA 110 is
CC almost identical to that of USDA 123 (N82006) with single base change in
CC codon 139 which is GAC in USDA 110. The deduced protein sequences of the
CC two nodD-1 differ by one AA at position 139, which is Asp in USDA 110.
CC nodD-2 may be used to enhance competitiveness of strains for nodulation
CC and in the selective manipulation of nodulation host range of strains.
SQ Sequence 330 AA;

Query Match 56.1%; Score 46; DB 1; Length 330;
Best Local Similarity 50.0%; Pred. No. 1.13e+02;
Matches 4: Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db	111	lfrnvvur	118	
	111	111	111	111
QY	1	LFRAVITK	8	
RESULT	13			
ID	R90617	standard; Protein; 728 AA.		
AC	R90617;			
DE	29-JUN-1996	(first entry)		
DE	Sulfolobus solfataricus transferase for alpha, alpha-trehalose prodn.			
KW	transferase; amylase; Sulfolobus; production; alpha, alpha-trehalose;			
KW	malto-oligosaccharide; hydrolysis.			
OS	Sulfolobus solfataricus.			
PN	W09534642-A.			
PD	21-DEC-1995.			
PF	14-JUN-1995; J01189.			
PR	15-JUN-1994; JP-133354.			
PR	18-AUG-1994; JP-194223.			
PR	31-OCT-1994; JP-290394.			
PR	21-NOV-1994; JP-311185.			
PR	21-NOV-1994; JP-286917.			
PR	21-APR-1995; JP-120673.			
PA	(KIRI) KIRIN BEER KK.			
DR	WPI; 96-049671/05.			
DR	N-PSDB; T12323.			
PT	Sulfolobus spp. derived transferase and amylase - for production of			
PT	alpha, alpha-trehalose from malto-oligosaccharide(s)			
PT	Claim 74; Page 213-219; 357pp; Japanese.			
CC	The transferase is derived from Sulfolobus solfataricus. The transferase			
CC	acts on a saccharide having at least three sugar units, in which at least			
CC	three glucose units at the reducing end are alpha-1,4 linked, to			
CC	transform the alpha-1,4 linkages to alpha-1, alpha-1 linkages. The			
CC	transferase has a mol. wt. of 74 to 76 kDa. It is characterised by			
CC	working at pH 4.5-6.0 and at 60-80 deg.C. It has an isoelectric point			
CC	of 5.3-6.3 and retains at least 90 percent activity after 6 hrs. at 80			
CC	deg.C. It is completely inhibited by 5 mM copper sulphate. Use of the			
CC	transferase and an amylase in succession on suitable substrates such			
CC	a malto-oligosaccharides, is useful for the production of			
CC	alpha, alpha-trehalose.			
CC	Sequence 728 AA;			
CC	Sequence 728 AA;			

Query Match	56.1%;	Score 46;	DB 17;	Length 728;
Best Local Similarity	33.3%;	Pred. No. 1.13e+02;		
Matches	4;	Conservative	5;	Mismatches 3;
			Indels 0;	Gaps 0;

```

Db      676 lfspivtreve 687
        ||::||:
Ov      1 LFRAVITKKVAD 12

```

RESULT	14
ID	R60900 standard; Protein; 159 AA.
AC	R60900;
AD	R60900;
DE	25-MAY-1995 (first entry)
DT	Borrelia VSDA antigen vaccine.
DR	OspC antigen; vaccine; Lyme disease
KW	serovar typing; restriction fragment
KW	RFLP; Pichia pastoris; ss.
KW	Borrelia burgdorferi VSDA.
OS	W09425596-A.
PN	

PD 10-NOV-1994. E01365.
 PF 29-APR-1994; US-053863.
 PR 29-APR-1993; US-053863.
 PA (IMMO) IMMUNO AG.
 PI Crowe B, Dörner F, Livey I;
 DR WPI; 94-358273/44.
 DR N-PSDB; Q73873.
 PT Immunogenic composition comprising OspC antigens - for the
 PT treatment of Lyme borreliosis in different, specific geographical
 PT areas.
 PS Disclosure; Fig. 9a; 115pp; English.
 CC A vaccine for Lyme disease includes selected OspC antigen
 CC formulations based on defined OspC families resolved by serovar
 CC typing and RFLP typing. Partial sequences of OspC genes selected
 CC from different RFLP types are given in Q73883-905 (encoded peptides,
 CC comprising the first 92% of mature OspC, are given in R62771-93).
 CC Complete sequences of these novel ospC genes, including the 3' end,
 CC plus sequences for the ospC genes of Borrelia strains H13 and 28691
 CC are given in Q73857-82, and encoded proteins in R60884-909. The
 CC DNA sequences may be expressed in e.g. Pichia pastoris for
 CC recombinant antigen production.
 SQ Sequence 159 AA;

Query Match 54.9%; Score 45; DB 12; Length 159;
 Best Local Similarity 55.6%; Pred. No. 1.45e+02;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 23 twiskitd 31
 :||:||||:
 QY 4 AVITKQVAD 12

RESULT 15
 ID R60908 standard; Protein; 173 AA.
 AC R60908;
 DT 25-MAY-1995 (first entry)
 DE Borrelia PBI antigen vaccine.
 KW ospc antigen; vaccine; Lyme disease; borreliosis; immunogen;
 KW serovar typing; restriction fragment length polymorphism;
 KW RFLP; Pichia pastoris.
 OS Borrelia burgdorferi PBI.
 PN W09425596-A.
 PD 10-NOV-1994.
 PF 29-APR-1994; E01365.
 PR 29-APR-1993; US-053863.
 PA (IMMO) IMMUNO AG.
 PI Crowe B, Dörner F, Livey I;
 DR WPI; 94-358273/44.
 DR N-PSDB; Q73881.
 PT Immunogenic composition comprising OspC antigens - for the
 PT treatment of Lyme borreliosis in different, specific geographical
 PT areas.
 PS Disclosure; Fig. 9a; 115pp; English.
 CC A vaccine for Lyme disease includes selected OspC antigen
 CC formulations based on defined OspC families resolved by serovar
 CC typing and RFLP typing. Partial sequences of OspC genes selected
 CC from different RFLP types are given in Q73883-905 (encoded peptides,
 CC comprising the first 92% of mature OspC, are given in R62771-93).
 CC Complete sequences of these novel ospC genes, including the 3' end,
 CC plus sequences for the ospC genes of Borrelia strains H13 and 28691

CC are given in Q73857-82, and encoded proteins in R60884-909. The
 CC DNA sequences may be expressed in e.g. Pichia pastoris for
 CC recombinant antigen production.
 SQ Sequence 173 AA;

Query Match 54.9%; Score 45; DB 12; Length 173;
 Best Local Similarity 55.6%; Pred. No. 1.45e+02;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 23 twiskitd 31
 :||:||||:
 QY 4 AVITKQVAD 12

Search completed: Thu Apr 3 11:58:53 1997
 Job time : 8 secs.

 WIPSELEH

 (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Thu Apr 3 11:58:17 1997; MaaPar time 2.53 Seconds
 122.180 Million cell updates/sec

Tabular output not generated.

Title: >US-08-190-411A-3
 Description: (1-12) from 5541104.pep
 Perfect Score: 82
 Sequence: 1 LFRVITKQVAD 12

Scoring table: PAM 150
 Gap 15

Searched: 82182 seqs, 25727515 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database:

pir48
 1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4
 8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unenc
 14:unrev

Statistics: Mean 24.518; Variance 36.713; scale 0.668

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Length	ID	Description	Pred. No.
1	82	100.0	280	12	tumor-associated ant	2.72e-05
2	54	63.9	693	11	ubiquitin-like fusio	7.17e+00
3	54	63.9	701	11	ubiquitin-like fusio	7.17e+00
4	54	63.9	885	9	anaphase spindle elo	7.17e+00
5	52	63.4	124	9	hypothetical protein	1.56e+01
6	52	63.4	317	12	tumor-associated ant	1.56e+01
7	52	63.4	489	10	ATP-dependent RNA he	1.56e+01
8	51	62.2	736	10	regulatory protein C	2.29e+01
9	51	62.2	980	9	BEM1 protein-binding	2.29e+01
10	51	62.2	980	9	BOB1 protein - yeast	2.29e+01
11	51	62.2	1729	10	hypothetical protein	2.29e+01
12	50	61.0	348	9	pheromone receptor -	3.35e+01
13	50	61.0	394	3	finM protein - Diche	3.35e+01
14	50	61.0	2560	8	peptide-synthetase 2	3.35e+01
15	49	59.8	224	3	ULI protein - human	4.85e+01
16	49	59.8	274	1	succinylidiaminopimel	4.85e+01
17	49	59.8	274	1	tetrahydrodipicolina	4.85e+01
18	49	59.8	303	4	tetrahydrodipicolina	4.85e+01
19	49	59.8	468	12	UDPGlucose 6-dehydro	4.85e+01
20	49	59.8	475	12	fatty acid beta-oxid	4.85e+01
21	49	59.8	528	10	[RNA-polymerase]-sub	4.85e+01
22	49	59.8	660	8	hypothetical protein	4.85e+01
23	49	59.8	1258	11	myosin-light-chain k	4.85e+01
24	49	59.8	1494	9	hypothetical protein	4.85e+01
25	48	58.5	320	10	stress-inducible pro	7.00e+01
26	48	58.5	516	9	radial spoke protein	7.00e+01
27	48	58.5	516	9	radial spoke protein	7.00e+01
28	48	58.5	578	8	amylase, BLMA - Bac	7.00e+01
29	48	58.5	580	8	amylase, maltogenic	7.00e+01
30	47	57.3	149	8	ribosomal protein L9	1.00e+02
31	47	57.3	173	2	alpha-crystallin cha	1.00e+02
32	47	57.3	173	2	alpha-crystallin cha	1.00e+02
33	47	57.3	249	5	histone H1 - fruit f	1.00e+02
34	47	57.3	249	5	histone H1 - fruit f	1.00e+02
35	47	57.3	301	9	mt2 protein - fissi	1.00e+02
36	47	57.3	309	10	coagulation factor G	1.00e+02
37	47	57.3	333	6	GTP-binding regulato	1.00e+02
38	47	57.3	335	6	GTP-binding regulato	1.00e+02
39	47	57.3	359	14	phospholipase C-acti	1.00e+02
40	47	57.3	359	2	GTP-binding regulato	1.00e+02
41	47	57.3	359	2	GTP-binding regulato	1.00e+02
42	47	57.3	360	7	GTP-binding regulato	1.00e+02
43	47	57.3	370	6	basal body P-ring pr	1.00e+02
44	47	57.3	628	14	pyruvate synthase (E	1.00e+02
45	47	57.3	775	12	protein kinase kem (1.00e+02

ALIGNMENTS

RESULT	1	JC2358	#type complete
ENTRY		tumor-associated antigen, MAGE-1 - human	
TITLE			

ORGANISM #formal_name Homo sapiens #common name man
DATE 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 15-Mar-1996

ACCESSIONS JC2358
REFERENCE JC2358

#authors Ding, M.; Beck, R.J.; Keller, C.J.; Fenton, R.G.
#journal Biochem. Biophys. Res. Commun. (1994) 202:549-555
#title Cloning and analysis of MAGE-1-related genes.

#accession JC2358
#molecule_type mRNA
#residues 1-280 #label DIN
#experimental_source melanoma cell line DM150

GENETICS
#gene MAGE

FEATURE
161-169 #region HLA-A1 binding #status predicted

SUMMARY
#length 280 #molecular-weight 30932 #checksum 467

Query Match 100.0%; Score 82; DB 12; Length 280;
Best Local Similarity 100.0%; Pred. No. 2.72e-05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 97 lfravttkvad 108.

QY 1 LFRVITTKVAD 12

RESULT 2

ENTRY JC2358 #type complete
TITLE ubiquitin-like fusion protein Ania - African clawed frog
ORGANISM #formal_name Xenopus laevis #common name African clawed frog
DATE 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 27-Jan-1995

ACCESSIONS JC2358

REFERENCE Linnen, J.M.; Bailey, C.P.; Weeks, D.L.
#authors Gene (1993) 128:181-188

#journal Two related localized mRNAs from Xenopus laevis encode
#title ubiquitin-like fusion proteins.

#accession JC2358

#molecule_type mRNA
#residues 1-693 #label LIN
#note nucleotide sequence is not given

GENETICS Ania

#gene #superfamily ubiquitin homology
CLASSIFICATION fusion protein; zinc; zinc finger

KEYWORDS 28-103 #region ubiquitin-like protein\
FEATURE #domain ubiquitin homology #label UBH
28-103 #region zinc finger motif
625-693 #length 693 #molecular-weight 76844 #checksum 7105

SUMMARY

Query Match 65.9%; Score 54; DB 11; Length 693;
Best Local Similarity 50.0%; Pred. No. 7.17e+00;

Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 474 lfrsvevriiad 485

QY 1 LFRVITTKVAD 12

```

RESULT 3
ENTRY   JN0674      #type complete
TITLE   ubiquitin-like fusion protein Anlb - African clawed frog
ORGANISM   #formal name Xenopus laevis #common name African clawed frog
DATE      24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change
          27-Jan-1995

ACCESSIONS
REFERENCE JN0673
#authors  Linnen, J.M.; Bailey, C.P.; Weeks, D.L.
#journal  Gene (1993) 128:181-188
#title    Two related localized mRNAs from Xenopus laevis encode
          ubiquitin-like fusion proteins.

#accession JN0674
#molecule_type mRNA
#residues  1-701 #label LIN
#note      nucleotide sequence is not given

GENETICS
#gene      Anlb
CLASSIFICATION
KEYWORDS   #superfamily ubiquitin homology
           fusion protein; zinc; zinc finger
FEATURE    #region ubiquitin-like protein\
28-103     #domain ubiquitin homology #label UBRV\
28-103     #region zinc finger motif
633-701    #length 701 #molecular-weight 78581 #checksum 3367
SUMMARY

Query Match 65.9%; Score 54; DB 11; Length 701;
Best Local Similarity 50.0%; Pred. No. 7.17e+00;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 481 lfrsvevrniad 492
    |||:| :||
Qy 1 LFRVITKQVAD 12

RESULT 4
ENTRY   S59660      #type complete
TITLE   anaphase spindle elongation protein ASE1 - yeast
          (Saccharomyces cerevisiae)
ORGANISM #formal name Saccharomyces cerevisiae
DATE      13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change
          09-Mar-1996

ACCESSIONS
REFERENCE S59660
#authors  Pellman, D.; Fink, G.R.
#submission submitted to the EMBL Data Library, January 1995
#description Yeast microtubule-associated proteins required for anaphase
          spindle elongation.

#accession S59660
#molecule_type DNA
#residues  1-885 #label PEL
#cross-references EMBL:U20235

GENETICS
#gene      ASE1
#map_position 15
SUMMARY   #length 885 #molecular-weight 101623 #checksum 8781

Query Match 65.9%; Score 54; DB 9; Length 885;

```

```

Best Local Similarity 60.0%; Pred. No. 7.17e+00;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 328 fksvltkxvs 337
    |::|::|
Qy 2 FRAVITKQVA 11

RESULT 5
ENTRY   S45156      #type complete
TITLE   hypothetical protein HRB124 - yeast (Saccharomyces
          cerevisiae)
ORGANISM #formal name Saccharomyces cerevisiae
DATE      31-Mar-1992 #sequence_revision 14-Sep-1994 #text_change
          14-Sep-1994

ACCESSIONS
REFERENCE S45156
          S45146
#authors  Vandenbol, M.; Durand, P.; Dion, C.; Bolle, P.; Portetelle,
          D.; Hilger, F.
#submission submitted to the EMBL Data Library, June 1994
#description Sequence analysis of a 40.1 kb DNA fragment located near the
          left telomere of yeast chromosome X.

#accession S45156
#molecule_type DNA
#residues  1-124 #label VAN
#cross-references EMBL:Z34098

GENETICS
#map_position 10L
SUMMARY   #length 124 #molecular-weight 14631 #checksum 4119

Query Match 63.4%; Score 52; DB 9; Length 124;
Best Local Similarity 41.7%; Pred. No. 1.56e+01;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 61 lfrtvvdhqvnn 72
    |||::|:|
Qy 1 LFRVITKQVAD 12

RESULT 6
ENTRY   JC2359      #type complete
TITLE   tumor-associated antigen , MAGE-X2 - human
ORGANISM #formal name Homo sapiens #common name man
DATE      20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
          15-Mar-1996

ACCESSIONS
REFERENCE JC2359
          JC2358
#authors  Ding, M.; Beck, R.J.; Keller, C.J.; Fenton, R.G.
#journal  Biochem. Biophys. Res. Commun. (1994) 202:549-555
#title    Cloning and analysis of MAGE-1-related genes.

#accession JC2359
#molecule_type mRNA
#residues  1-317 #label DIN
#experimental_source melanoma cell line DM150

GENETICS
#gene      MAGE-X2
#map_position 317
SUMMARY   #region HLA-A1 binding #status predicted
          #length 317 #molecular-weight 34928 #checksum 9004

```

Query Match 63.4%; Score 52; DB 12; Length 317;
Best Local Similarity 41.7%; Pred. No. 1.56e+01;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 105 lfrealankvde 116
||| :||| :
QY 1 LFRVITKKVAD 12

RESULT 7
ENTRY S40731 #type complete
TITLE ATP-dependent RNA helicase homolog T26G10.1-- Caenorhabditis elegans
ORGANISM #formal name Caenorhabditis elegans
DATE 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Feb-1996

ACCESSIONS S40731
REFERENCE S40731
#authors Berks, M.
#submission submitted to the EMBL Data Library, December 1993
#accession S40731
#molecule_type DNA
#residues 1-489 ##label BER
#cross-references EMBL:229115

GENETICS
#introns 26/1; 319/3; 403/1
SUMMARY #length 489 #molecular-weight 54227 #checksum 4937

Query Match 63.4%; Score 52; DB 10; Length 489;
Best Local Similarity 63.6%; Pred. No. 1.56e+01;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 223 lfsatmttkvs 233
||| :||| :
QY 1 LFRVITKKVA 11

RESULT 8
ENTRY A27477 #type complete
TITLE regulatory protein CLS4 - yeast (Saccharomyces cerevisiae)
ALTERNATE_NAMES cell division control protein CDC24; protein YAL041
ORGANISM #formal name Saccharomyces cerevisiae
DATE 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 01-Sep-1995

ACCESSIONS A27477
REFERENCE A27477
#authors Miyamoto, S.; Ohya, Y.; Ohsumi, Y.; Anraku, Y.
#journal Gene (1987) 54:125-132
#title Nucleotide sequence of the CLS4 (CDC24) gene of Saccharomyces cerevisiae.

#cross-references M01D:87277425
#accession A27477
#molecule_type DNA
#residues 1-736 ##label MIY
#cross-references GB:M16809

REFERENCE S51956
#authors Bussey, H.; Kaback, D.B.; Zhong, W.; Vo, D.T.; Clark, M.W.; Fortin, N.; Hall, J.; Ouellette, B.F.; Keng, T.; Barton, A.B.; Su, Y.; Davies, C.K.; Storms, R.K.
#submission submitted to the EMBL Data Library, August 1994

#description The sequence of chromosome 1 of Saccharomyces cerevisiae.
#accession S51978
#molecule_type DNA
#residues 1-736 ##label BUS
#cross-references EMBL:U12980

GENETICS
#gene LISTA:CLS4; CDC24
#map_position 1L
SUMMARY #length 736 #molecular-weight 83960 #checksum 4670

Query Match 62.2%; Score 51; DB 10; Length 736;
Best Local Similarity 63.6%; Pred. No. 2.29e+01;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Db 399 lfsevttkksa 409
||| :||| :
QY 1 LFRVITKKVA 11

RESULT 9
ENTRY S45444 #type complete
TITLE BEM1 protein-binding protein BOB1 - yeast (Saccharomyces cerevisiae)
ALTERNATE_NAMES protein YBL0717; protein YBL085w
ORGANISM #formal name Saccharomyces cerevisiae
DATE 09-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 09-Sep-1994

ACCESSIONS S45444; S45421; S45826
REFERENCE S45444
#authors Bender, A.; Bender, L.; Kokojan, V.
#submission submitted to the EMBL Data Library, April 1994
#description Yeast Boblp (Bemlp-binding protein) binds to the SH3 domain-containing protein Bemlp.

#accession S45444
#molecule_type DNA
#residues 1-980 ##label BEN
#cross-references EMBL:L31406

REFERENCE S45387
#authors Obermaier, B.; Gassenhuber, J.; Piravandi, E.; Domdey, H.
#submission submitted to the EMBL Data Library, May 1994
#description Sequence analysis of a 78,6 kb segment of the left end of Saccharomyces cerevisiae chromosome II.

#accession S45421
#molecule_type DNA
#residues 1-980 ##label OBE
#cross-references EMBL:X79489

REFERENCE S45816
#authors Domdey, H.; Gassenhuber, H.; Obermaier, B.; Piravandi, E.
#submission submitted to the Protein Sequence Database, August 1994
#accession S45826
#molecule_type DNA
#residues 1-980 ##label DOM
#cross-references EMBL:Z35846

GENETICS
#gene BOB1
#map_position 2L
CLASSIFICATION #superfamily SH3 homology
FEATURE
20-72 #domain SH3 homology #label SH3
SUMMARY #length 980 #molecular-weight 109294 #checksum 8660

Query Match 62.2%; Score 51; DB 9; Length 980;
Best Local Similarity 54.5%; Pred. No. 2.29e+01;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 66 lypavftkria 76

l:||||:|

QY 1 LFRVITKVA 11

RESULT 10
ENTRY BOB1 protein - yeast (Saccharomyces cerevisiae)
TITLE protein YBL0717
ALTERNATE_NAMES #formal name Saccharomyces cerevisiae
ORGANISM 15-feb-1996 #sequence_revision 01-Mar-1996 #text_change
DATE 01-Mar-1996
ACCESSIONS S59218
REFERENCE S59184
#authors Obermaier, B.; Gassenhuber, J.; Piravandi, E.; Domdey, H.
#journal Yeast (1995) 11:1103-1112
#title Sequence analysis of a 78.6 kb segment of the left end of
Saccharomyces cerevisiae chromosome II.
#accession S59218
#molecule_type DNA
#residues 1-980 #label OBE
#cross-references EMBL:X79489
#note the nucleotide sequence was submitted to the EMBL Data
Library, May 1994
#note neither amino acid nor nucleotide sequence is given

GENETICS
#gene BOB1
#map_position 2L
SUMMARY #length 980 #molecular-weight 109294 #checksum 8660

Query Match 62.2%; Score 51; DB 9; Length 980;
Best Local Similarity 54.5%; Pred. No. 2.29e+01;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 66 lypavftkria 76

l:||||:|

QY 1 LFRVITKVA 11

RESULT 11
ENTRY S57596
TITLE hypothetical protein YM9959.11c - yeast (Saccharomyces cerevisiae)
ORGANISM #formal name Saccharomyces cerevisiae
DATE 19-Oct-1995 #sequence_revision 03-Nov-1995 #text_change
10-Nov-1995
ACCESSIONS S57596
REFERENCE S57587
#authors Skelton, J.; Churcher, C.M.
#submission submitted to the EMBL Data Library, June 1995
#accession S57596
#molecule_type DNA
#residues 1-1729 #label SKE
#cross-references EMBL:249939
#experimental_source strain AB972

GENETICS

#map_position 13R
SUMMARY #length 1729 #molecular-weight 193132 #checksum 3679
Query Match 62.2%; Score 51; DB 10; Length 1729;
Best Local Similarity 54.5%; Pred. No. 2.29e+01;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 1674 lferiitkkit 1684

l:||||:|

QY 1 LFRVITKVA 11

RESULT 12
ENTRY S18521
TITLE pheromone receptor - fission yeast (Schizosaccharomyces pombe)
ORGANISM #formal name Schizosaccharomyces pombe
DATE 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change
30-Sep-1993
ACCESSIONS S18521; S16732
REFERENCE S18521
#authors Kitamura, K.; Shimoda, C.
#journal EMBO J. (1991) 10:3743-3751
#title The Schizosaccharomyces pombe mam2 gene encodes a putative
pheromone receptor which has a significant homology with
the Saccharomyces cerevisiae Ste2 protein.

#cross-references MUID:92037537
#accession S18521
#molecule_type DNA
#residues 1-348 #label KIT
SUMMARY #length 348 #molecular-weight 39285 #checksum 3454

Query Match 61.0%; Score 50; DB 9; Length 348;
Best Local Similarity 55.6%; Pred. No. 3.35e+01;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 229 lfrailirk 237

l:||||:|

QY 1 LFRVITKK 9

RESULT 13
ENTRY YOB2DH
TITLE fimD protein - Dichelobacter nodosus (serotype H1)
ORGANISM #formal name Dichelobacter nodosus
DATE 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
31-Mar-1993
ACCESSIONS S15255
REFERENCE S15240
#authors Hobbs, M.; Dalrymple, B.P.; Cox, P.T.; Livingstone, S.P.;
DeLaney, S.F.; Mattick, J.S.
#journal Mol. Microbiol. (1991) 5:543-560
#title Organization of the fimbral gene region of Bacteroides
nodosus: class I and class II strains.

#cross-references MUID:91260439
#accession S15255
#molecule_type DNA
#residues 1-394 #label HOB

```

##cross-references EMBL:X52390
##note the source is designated as Bacteroides nodosus

GENETICS
#gene fmd
#start codon GTG
CLASSIFICATION #superfamily fmd protein
KEYWORDS fimbria
SUMMARY #length 394 #molecular-weight 45105 #checksum 2838

Query Match 61.0%; Score 50; DB 3; Length 394;
Best Local Similarity 72.7%; Pred. No. 3.35e+01;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 365 fraastkktad 375
   ||| ||| ||
Qy 2 FRAVITKKVAD 12

RESULT 14
ENTRY S49134 #type complete
TITLE peptide-synthetase 2 - Bacillus subtilis
ORGANISM #formal_name Bacillus subtilis
DATE 16-Feb-1995 #sequence_revision 12-May-1995 #text_change
      21-Jul-1995

ACCESSIONS S49134
REFERENCE S49131
#authors Tognoni, A.; Grandi, G.
#description Bacillus subtilis genome project, DNA sequence from gita to
              citB; part 1: sequence at 175 degrees.
#accession S49134
#status preliminary
#molecule_type DNA
#residues 1-2560 #label TOG
##cross-references EMBL:234883
CLASSIFICATION #superfamily gramicidin S synthetase I repeat homology; acyl
              carrier protein homology

FEATURE
456-1036 #domain gramicidin S synthetase I repeat homology #label
          GRS1\
968-1036 #domain acyl carrier protein homology #label ACPI\
1486-2076 #domain gramicidin S synthetase I repeat homology #label
          GRS2\

2009-2076 #domain acyl carrier protein homology #label ACP2
SUMMARY #length 2560 #molecular-weight 290162 #checksum 9702

Query Match 61.0%; Score 50; DB 8; Length 2560;
Best Local Similarity 41.7%; Pred. No. 3.35e+01;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 63 ifrtifikevpd 74
   ||::: |||
Qy 1 LFRVITKKVAD 12

RESULT 15
ENTRY WMBE8G #type complete
TITLE ULI protein - human herpesvirus 2 (strain HG52)
ORGANISM #formal_name human herpesvirus 2
          host Homo sapiens (man)
#note

```

```

DATE 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change
      08-Apr-1994
ACCESSIONS JQ1494
REFERENCE JQ1494
#authors McGeoch, D.J.; Cunningham, C.; McIntyre, G.; Dolan, A.
#journal J. Gen. Virol. (1991) 72:3057-3075
#title Comparative sequence analysis of the long repeat regions and
        adjoining parts of the long unique regions in the genomes
        of herpes simplex viruses types 1 and 2.
##cross-references MUID:92113549
#accession JQ1494
#molecule_type DNA
#residues 1-224 #label MCG
##cross-references DDBJ:D01127

GENETICS ULI
#gene #superfamily varicella-zoster virus gene 60 protein
CLASSIFICATION #length 224 #molecular-weight 25192 #checksum 2478
SUMMARY

Query Match 59.8%; Score 49; DB 3; Length 224;
Best Local Similarity 50.0%; Pred. No. 4.85e+01;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 27 vlrsviakevqd 38
   ::|||: ||
Qy 1 LFRVITKKVAD 12

Search completed: Thu Apr 3 11:58:26 1997
Job time : 9 secs.

*****

VIRUS

*****

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MParch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Apr 3 11:57:52 1997; MasPar time 1.81 Seconds
Tabular output not generated.

Title: >US-08-190-411A-3
Description: (1-12) from 5541104.pep
Perfect Score: 82
Sequence: 1 LFRVITKKVAD 12

Scoring table: PAM 150
               Gap 15

```

Searched: 52205 seqs, 18531385 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot33

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10

Statistics: Mean 25.775; Variance 29.272; scale 0.881

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	82	100.0	309	5	MAG1_HUMAN	MELANOMA-ASSOCIATED A	1.56e+07
2	60	73.2	124	5	MAG5_HUMAN	MELANOMA-ASSOCIATED A	5.41e-02
3	52	63.4	317	5	MAG4_HUMAN	MELANOMA-ASSOCIATED A	3.08e+00
4	52	63.4	489	10	YN21_CAEEL	PUTATIVE ATP-DEPENDENT	3.08e+00
5	51	62.2	234	5	MAG8_HUMAN	MELANOMA-ASSOCIATED A	4.95e+00
6	51	62.2	854	2	CC24_YEAST	CELL DIVISION CONTROL	4.95e+00
7	51	62.2	980	1	BOB1_YEAST	BOB1 PROTEIN (BEMI-BI)	4.95e+00
8	50	61.0	348	5	MAM2_SCHPO	PEROMYXIN P-FACTOR RE	7.89e+00
9	50	61.0	367	10	YOJO_ECOLI	HYPOTHETICAL 41.2 KD	7.89e+00
10	50	61.0	394	3	FMDH_BACNO	POSSIBLE FIMBRIAL ASS	7.89e+00
11	50	61.0	690	1	BEL1_YEAST	BIOTIN APO-PROTEIN LI	7.89e+00
12	50	61.0	2560	7	PPS2_BACSU	PEPTIDE SYNTHETASE 2.	1.25e+01
13	49	59.8	224	9	UL01_HSV2H	GLYCOPROTEIN L PRECUR	1.25e+01
14	49	59.8	274	3	DAPD_ECOLI	2,3,4,5-TETRAHYDROXYR	1.25e+01
15	49	59.8	274	3	DAPD_ECOLI	2,3,4,5-TETRAHYDROXYR	1.25e+01
16	49	59.8	275	3	DAPD_HAEIN	2,3,4,5-TETRAHYDROXYR	1.25e+01
17	49	59.8	1258	2	CTK1_YEAST	CTD KINASE ALPHA SUBU	1.25e+01
18	49	59.8	149	8	RL9_HAEIN	MYOSIN LIGHT CHAIN KI	1.25e+01
19	48	58.5	320	8	ST35_FUSOX	STRESS-INDUCIBLE PROT	1.96e+01
20	48	58.5	424	3	FADH_METMR	GLUTATHIONE-DEPENDENT	1.96e+01
21	48	58.5	516	8	RSP3_CHLRE	RADIAL SPOKE PROTEIN	1.96e+01
22	48	58.5	578	1	AMYM_BACLI	MALTOGENIC ALPHA-AMYL	1.96e+01
23	48	58.5	754	10	YAJ3_SCHPO	PUTATIVE ATP-DEPENDEN	1.96e+01
24	47	57.3	149	8	RL9_HAEIN	50S RIBOSOMAL PROTEIN	3.06e+01
25	47	57.3	173	2	CRAA_CERSI	ALPHA CRYSTALLIN A CH	3.06e+01
26	47	57.3	173	2	CRAA_PIG	ALPHA CRYSTALLIN A CH	3.06e+01
27	47	57.3	173	2	CRAA_MUSVI	ALPHA CRYSTALLIN A CH	3.06e+01
28	47	57.3	173	2	CRAA_EULFU	ALPHA CRYSTALLIN A CH	3.06e+01
29	47	57.3	173	2	CRAA_PERPO	ALPHA CRYSTALLIN A CH	3.06e+01
30	47	57.3	225	9	UL92_EBV	HYPOTHETICAL PROTEIN	3.06e+01
31	47	57.3	249	4	H1_DROHY	HISTONE H1.	3.06e+01
32	47	57.3	301	6	NMT2_SCHPO	NMT2 PROTEIN.	3.06e+01
33	47	57.3	314	5	MAG3_HUMAN	MELANOMA-ASSOCIATED A	3.06e+01
34	47	57.3	353	4	GBQ_DROME	GUANINE NUCLEOTIDE-BI	3.06e+01
35	47	57.3	353	4	GBQ_MOUSE	GUANINE NUCLEOTIDE-BI	3.06e+01
36	47	57.3	354	4	GBQ_LOLFO	GUANINE NUCLEOTIDE-BI	3.06e+01
37	47	57.3	355	4	GB14_MOUSE	GUANINE NUCLEOTIDE-BI	3.06e+01
38	47	57.3	359	4	GB11_MOUSE	GUANINE NUCLEOTIDE-BI	3.06e+01
39	47	57.3	359	4	GB11_HUMAN	GUANINE NUCLEOTIDE-BI	3.06e+01

40 47 57.3 359 4 GB11_MELGA GUANINE NUCLEOTIDE-BI 3.06e+01
41 47 57.3 370 3 FLGI_CAOCR FLAGELLAR P-RING PROT 3.06e+01
42 47 57.3 401 1 ALKB_PSEOL ALKANE-1 MONOOXYGENAS 3.06e+01
43 47 57.3 441 3 FUS6_ARATH FUSCA PROTEIN FUS6. 3.06e+01
44 47 57.3 774 5 KEMK_MOUSE PUTATIVE SERINE/THREO 3.06e+01
45 47 57.3 1450 8 RPO1_ASFB7 DNA-DIRECTED RNA POLY 3.06e+01

ALIGNMENTS

RESULT	1	MAG1_HUMAN	STANDARD;	PRT;	309 AA.
ID	P43355;				
AC	01-NOV-1995 (REL. 32, CREATED)				
DT	01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)				
DT	01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)				
DE	MELANOMA-ASSOCIATED ANTIGEN 1 (MAGE-1 ANTIGEN) (ANTIGEN M22-E).				
GN	MAGE1.				
OS	HOMO SAPIENS (HUMAN).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
OC	EUTHERIA; PRIMATES.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 92086861.				
RA	VAN DER BRUGEN P., TRAVERSARI C., CHOMEZ P., LORQUIN C., DE PLAEN E.,				
RA	VAN DEN EYNDE B., KNUTH A., BOON T.;				
RL	SCIENCE 254:1643-1647(1991).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=SKIN;				
RX	MEDLINE; 94311935.				
RA	DING M., BECK R.J., KELLER C.J., FENTON R.G.;				
RL	BIOCHEM. BIOPHYS. RES. COMMUN. 202:549-555(1994).				
RN	[3]				
RP	MUTAGENESIS.				
RC	TISSUE=Blood;				
RX	MEDLINE; 94157413.				
RA	GAUGLER B., VAN DEN EYNDE B., VAN DER BRUGEN P., ROMERO P.,				
RA	GAFORIO J., DE PLAEN E., LETHE B., BRASSEUR F., BOON T.;				
RL	J. EXP. MED. 179:921-930(1994).				
CC	!- FUNCTION: NOT KNOWN, THOUGH MAY PLAY A ROLE IN EMBRYONAL				
CC	DEVELOPMENT AND TUMOR TRANSFORMATION OR ASPECTS OF TUMOR				
CC	PROGRESSION. ANTIGEN RECOGNIZED ON A MELANOMA BY AUTOLOGOUS				
CC	CYTOLYTIC T LYMPHOCYTES.				
CC	!- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES,				
CC	SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LUNG				
CC	CARCINOMA AND BREAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT				
CC	FOR TESTES. NEVER EXPRESSED IN KIDNEY TUMORS, LEUKEMIAS AND				
CC	LYMPHOMAS.				
CC	!- POLYMORPHISM: THE VARIANT AT POSITION 32 LIKELY REPRESENTS A				
CC	POLYMORPHISM OF THE MAG-1 GENE.				
CC	!- SIMILARITY: BELONGS TO THE MAGE FAMILY.				
CC	EMBL; M77481; G416115; -.				
DR	MIM; 600186; 11TH EDITION.				
KW	ANTIGEN; MULTIGENE FAMILY; POLYMORPHISM; TUMOR ANTIGEN.				
FT	VARIANT 32 32 T -> A.				
FT	DOMAIN 33 36 POLY-SER.				
FT	MUTAGEN 163 163 D->A: ABOLISHES HLA-A1 BINDING.				
FT	MUTAGEN 169 169 Y->A: ABOLISHES HLA-A1 BINDING.				
SQ	SEQUENCE 309 AA; 34342 MW; E6CB1300 CRC32;				

Query Match 100.0%; Score 82; DB 5; Length 309;
Best Local Similarity 100.0%; Pred. No. 1.56e-07;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 97 lfraftvikkvad 108
|||||||
Qy 1 LFRVITKKVAD 12

RESULT 2
ID MAG5 HUMAN STANDARD; PRT; 124 AA.
AC P43359;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE MELANOMA-ASSOCIATED ANTIGEN 5 (MAGE-5 ANTIGEN).
GN MAGE5.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95012457.
RA DE PLAEN E., ARDEN K., TRAVERSARI C., GAFORIO J.J., SZIKORA J.-P.,
RA BRASSEUR R., CHOMEZ P., DE BACKER O., CAVENEE W., BOON T.;
RL IMMUNOGENETICS 40:360-369(1994).
CC -!- FUNCTION: NOT KNOWN, THOUGH MAY PLAY A ROLE TUMOR TRANSFORMATION
OR PROGRESSION.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES,
CC SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LUNG
CC CARCINOMA AND BREAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT
CC FOR TESTES.
CC -!- SIMILARITY: BELONGS TO THE MAGE FAMILY.
DR EMBL; U10689; G533521; -;
DR EMBL; U10689; G533519; -;
KW ANTIGEN; MULTIGENE FAMILY. POLY-SER.
FT DOMAIN 40 43
SQ SEQUENCE 124 AA; 13015 MW; 7216B8C8 CRC32;

Query Match 73.2%; Score 60; DB 5; Length 124;
Best Local Similarity 66.7%; Pred. No. 5.41e-02;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 104 vfraalskkvad 115
|||||
Qy 1 LFRVITKKVAD 12

RESULT 3
ID MAG4 HUMAN STANDARD; PRT; 317 AA.
AC P43358;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE MELANOMA-ASSOCIATED ANTIGEN 4 (MAGE-4 ANTIGEN) (MAGE-X2).
GN MAGE4.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; PRIMATES.

RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-BLOOD;
RX MEDLINE; 95012457.
RA DE PLAEN E., ARDEN K., TRAVERSARI C., GAFORIO J.J., SZIKORA J.-P.,
RA DE SMET C., BRASSEUR F., VAN DER BRUGGEN P., LETHE B., LURQUIN C.,
RA BRASSEUR R., CHOMEZ P., DE BACKER O., CAVENEE W., BOON T.;
RL IMMUNOGENETICS 40:360-369(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE-SKIN;
RX MEDLINE; 94311935.
RA DING M., BECK R.J., KELLER C.J., FENTON R.G.;
RL BIOCHEM. BIOPHYS. RES. COMMUN. 202:549-555(1994).
CC -!- FUNCTION: NOT KNOWN, THOUGH MAY PLAY A ROLE IN EMBRYONAL
CC DEVELOPMENT AND TUMOR TRANSFORMATION OR ASPECTS OF TUMOR
CC PROGRESSION.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES,
CC SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LUNG
CC CARCINOMA AND BREAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT
CC FOR TESTES AND PLACENTA.
CC -!- SIMILARITY: BELONGS TO THE MAGE FAMILY. STRONG SIMILARITY WITH
CC MAGE-1.

DR EMBL; U10687; G533515; -;
DR EMBL; U10688; G533517; -;
DR EMBL; U10340; G499124; -;
KW ANTIGEN; MULTIGENE FAMILY; POLYMORPHISM; TUMOR ANTIGEN.
FT DOMAIN 41 44
FT VARIANT 173 173 T -> A.
FT CONFLICT 307 307 E -> Q (IN REF. 2).
SQ SEQUENCE 317 AA; 34929 MW; 3CE38AF9 CRC32;

Query Match 63.4%; Score 52; DB 5; Length 317;
Best Local Similarity 41.7%; Pred. No. 3.08e+00;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 105 lfrealnkvde 116
|||::|||
Qy 1 LFRVITKKVAD 12

RESULT 4
ID YN21 CAEEL STANDARD; PRT; 489 AA.
AC P34580;
DT 01-FEB-1994 (REL. 28, CREATED)
DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III.
GN T26G10.1.
OS CAENORHABDITIS ELEGANS.
OC EUKARYOTA; METAZOA; ACCELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-BRISTOL N2;
RX MEDLINE; 94150718.
RA WILSON R., AINSOUGH R., ANDERSON K., BAYNES C., BERKS M., COULSON A.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., FRASER A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FRASER A.,
RA FULTON L., GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M.,

RA JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISSTER N.,
RA LATREILLE P., LIGHTNING J., LLOYD C., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SIMS M., SWALDON N., SMITH A., SMITH M., SONNHAMMER E., STADEN R.,
RA SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K.,
RA WATERSON R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J.,
RA WOHLDMAN P.;
RL NATURE 368:32-38(1994).

CC -1- FUNCTION: PROBABLE ATP-BINDING RNA HELICASE.
CC -1- SIMILARITY: TO OTHER "DEAD" BOX FAMILY HELICASES.

DR EMBL; Z29115; G439260; -.
DR PIR; S40731; S40731.
DR WORMPEP; T26610.1; CR00337.
DR PROSITE; PS00039; DEAD ATP HELICASE.
KW HYPOTHETICAL PROTEIN; HELICASE; ATP-BINDING; RNA-BINDING.
FT DOMAIN 31 40
FT NP BIND 88 95 ASP/GLU-RICH (ACIDIC).
FT SITE 194 197 DEAD BOX.
FT DOMAIN 471 482 GLY-RICH.
SQ SEQUENCE 489 AA; 54227 MW; B9EFF81A CRC32;

Query Match 63.4%; Score 52; DB 10; Length 489;
Best Local Similarity 63.6%; Pred. No. 3.08e+00;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 223 lfsatmtkks 233
|||:||||
Qy 1 LFRVITKVA 11

RESULT 5
ID MAC8 HUMAN STANDARD; PRT; 234 AA.
AC P43361;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE MELANOMA-ASSOCIATED ANTIGEN 8 (MAGE-8 ANTIGEN).
GN MAGE8.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95012457.
RA DE PLAEN E., ARDEN K., TRAVERSARI C., GAFORIO J.J., SZIKORA J.-P.,
RA DE SNET C., BRASSEUR F., VAN DER BRUGGEN P., LETHE B., LORQUIN C.,
RA BRASSEUR R., CHOMEZ P., DE BACKER O., CAVEENE W., BOON T.;
RL IMMUNOGENETICS 40:360-369(1994).

CC -1- FUNCTION: NOT KNOWN, THOUGH MAY PLAY A ROLE IN EMBRYONAL
CC DEVELOPMENT AND TUMOR TRANSFORMATION OR ASPECTS OF TUMOR
CC PROGRESSION.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES,
CC SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LUNG
CC CARCINOMA AND BREAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT
CC FOR TESTES AND PLACENTA.
CC -1- SIMILARITY: BELONGS TO THE MAGE FAMILY.
DR EMBL; U10693; G533526; -.
KW ANTIGEN; MULTIGENE FAMILY; TUMOR ANTIGEN.
FT DOMAIN 40 43
SQ SEQUENCE 234 AA; 25197 MW; D4931BC3 CRC32;

Query Match 62.2%; Score 51; DB 5; Length 234;
Best Local Similarity 50.0%; Pred. No. 4.95e+00;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Db 107 lfrealdkva 118
|||:||||
Qy 1 LFRVITKVA 12

RESULT 6
ID CC24 YEAST STANDARD; PRT; 854 AA.
AC P11433;
DT 01-OCT-1989 (REL. 12, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE CELL DIVISION CONTROL PROTEIN 24 (CALCIUM REGULATORY PROTEIN).
GN CDC24 OR CLS4 OR YAL041W.
OS SACHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 87277425.
RA MIYAMOTO S., OHYA Y., OHSUMI Y., ANRAKU Y.;
RL GENE 54:125-132(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-S288C / AB972;
RX MEDLINE; 95249563.
RA BUSSEY H., KABACK D.B., ZHONG W., VO D.T., CLARK M.W., FORTIN N.,
RA HALL J., OUELLETTE B.F.F., KENG T., BARTON A.B., SU Y., DAVIES C.K.,
RA STORMS R.K.;
RL PROC. NATL. ACAD. SCI. U.S.A. 92:3809-3813(1995).
RN [3]
RP SIMILARITY TO CDC24 FAMILY.

RX MEDLINE; 92095962.
RA MIYAMOTO S., OHYA Y., SANO Y., SAKAGUCHI S., IIDA H., ANRAKU Y.;
RL BIOCHEM. BIOPHYS. RES. COMMUN. 181:604-610(1991).
CC -1- FUNCTION: PROMOTES THE EXCHANGE OF CDC42-BOUND GDP BY GTP.
CC CONTROL THE CALCIUM REGULATORY PROCESS OF BUD EMERGENCE. CDC24 MAY
CC BE INVOLVED IN THE INITIAL SELECTION AND ORGANIZATION OF THE
CC BUDDING SITE.
CC -1- SIMILARITY: TO OTHER GUANINE-NUCLEOTIDE RELEASING FACTORS OF THE
CC CDC24 FAMILY.
CC -1- SIMILARITY: CONTAINS A PH DOMAIN.
DR EMBL; M16809; G1100997; -.
DR EMBL; U12980; G1101003; -.
DR PIR; A27477; A27477.
DR LISTA; SC00151; CDC24.
DR SGD; L0000262; CDC24.
DR PROSITE; PS00741; GDS CDC24.
DR PROSITE; PS50003; PH DOMAIN.
KW GUANINE-NUCLEOTIDE RELEASING FACTOR.
FT DOMAIN 478 668
FT DOMAIN 494 600 SER/THR-RICH.
FT DOMAIN 681 778 SER/THR-RICH.
SQ SEQUENCE 854 AA; 96939 MW; E74FC7DC CRC32;

Query Match 62.2%; Score 51; DB 2; Length 854;
Best Local Similarity 63.6%; Pred. No. 4.95e+00;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Db 517 lfsevtkkea 527
|| |::||| |
Qy 1 LFRVITKVA 11

RESULT 7
ID BOB1 YEAST STANDARD; PRT; 980 AA.
AC P38041;
DT 01-OCT-1994 (REL. 30, CREATED)
DT 01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE BOB1 PROTEIN (BEM1-BINDING PROTEIN).
GN BOB1 OR BOB1 OR YBL085W OR YBL0717.
OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN [1]
RP SEQUENCE FROM N.A.
RA BENDER A., BENDER L., KOKOJAN V.;
RL SUBMITTED (APR-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE; 96076635.
RA OBERWALTER B., GASSENHUBER J., PIRAVANDI E., DOMDEY H.;
RL YEAST 11:1103-1112(1995).
CC -|- FUNCTION: BINDS TO THE BEM1 PROTEIN.
CC -|- SIMILARITY: CONTAINS A COPY OF THE SH3 DOMAIN.
CC -|- SIMILARITY: CONTAINS A PH DOMAIN.
DR EMBL; L31406; G466436; -.
DR EMBL; X79489; G496694; -.
DR EMBL; Z35846; G536138; -.
DR PIR; S45444; S45444.
DR LISTA; SC00111; BOB1.
DR SGD; L0000191; BOB1.
DR PROSITE; P550002; SH3.
DR PROSITE; P550003; PH_DOMAIN.
DR SH3 DOMAIN.
KW SH3 DOMAIN. 13 77 SH3.
FT DOMAIN 776 895 PH.
FT SEQUENCE 980 AA; 109295 MW; 99B7E197 CRC32;
SQ

Query Match 62.2%; Score 51; DB 1; Length 980;
Best Local Similarity 54.5%; Pred. No. 4.95e+00;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 66 lypavtkria 76
|: |::||| |
Qy 1 LFRVITKVA 11

RESULT 8
ID MAM2 SCHEP STANDARD; PRT; 348 AA.
AC Q00619;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE PHEROMONE P-FACTOR RECEPTOR.
GN MAM2.

OS SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=975;
RX MEDLINE; 92037537.
RA KITAMURA K., SHIMODA C.;
RL EMBO J. 10:3743-3751(1991).
CC -|- FUNCTION: RECEPTOR FOR THE PEPTIDE PHEROMONE P-FACTOR, A MATING
CC -|- FACTOR OF S.POMBE. PHEROMONE SIGNALING IS ESSENTIAL FOR INITIATION
CC -|- OF MEIOSIS IN S.POMBE; P-FACTOR SIGNALING ALONE MAY BE SUFFICIENT.
CC -|- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -|- SIMILARITY: TO OTHER FUNGI G-LINKED RECEPTORS.
DR EMBL; X61672; G4978; -.
DR PIR; S18521; S18521.
DR GCRDB; GCR 0252; -.
DR TRANSMEMBRANE; G-PROTEIN COUPLED RECEPTOR; PHEROMONE RESPONSE.
KW TRANSMEM 46 69
FT TRANSMEM 79 103
FT TRANSMEM 125 141
FT TRANSMEM 162 180
FT TRANSMEM 207 225
FT TRANSMEM 249 267
FT TRANSMEM 283 301
SQ SEQUENCE 348 AA; 39285 MW; 68E94E15 CRC32;

Query Match 61.0%; Score 50; DB 5; Length 348;
Best Local Similarity 55.6%; Pred. No. 7.89e+00;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 229 lfrailirk 237
||||:| |
Qy 1 LFRVITKK 9

RESULT 9
ID YOJQ ECOLI STANDARD; PRT; 367 AA.
AC P47726;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 41.2 KD PROTEIN IN MICF-RCSB INTERGENIC REGION.
GN YOJQ.
OS ESCHERICHIA COLI.
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC ENTEROBACTERIACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / EMG2;
RA ROBISON K., ESTEP P.E., O'KEEFE T., CHURCH G.M.;
RL SUBMITTED (OCT-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; U38659; G1054952; -.
DR ECOGENE; EG13??; YOJQ.
KW HYPOTHETICAL PROTEIN; TRANSMEMBRANE.
FT TRANSMEM 170 190
FT SEQUENCE 367 AA; 41227 MW; 18962762 CRC32;
SQ

Query Match 61.0%; Score 50; DB 10; Length 367;
Best Local Similarity 60.0%; Pred. No. 7.89e+00;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 238 rtvisnkiaad 247
l:||||:||||
Qy 3 RAVITKKVAD 12

RESULT 10
ID FMDH BACNO STANDARD; PRT; 394 AA.
AC P1742i; 1990 (REL. 15, CREATED)
DT 01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
DT 01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
DT 01-MAR-1992 (REL. 21, LAST ANNOTATION UPDATE)
DE POSSIBLE FIMBRIAL ASSEMBLY PROTEIN FIMD (SEROGROUP H1).
GN FIMD.
OS BACTEROIDES NODOSUS (DICHELOBACTER NODOSUS).
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; ANAEROBIC RODS;
OC BACTEROIDACEAE.
FN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SEROGROUP H1 ISOLATE VCS1215;
RX MEDLINE; 91260439.
RA HOBBS M., DALRYMPLE B.P., COX P.T., LIVINGSTONE S.P., DELANEY S.F.,
RA MATTICK J.S.;
RL MOL. MICROBIOL. 5:543-560(1991).
DR EMBL; X52390; G580812; -.
DR FIR; S15255; YQBZDH.
DR PROSITE; PS00146; BETA_LACTAMASE_A.
KW FIMBRIA.
SQ SEQUENCE 394 AA; 45105 MW; 1310A727 CRC32;

Query Match 61.0%; Score 50; DB 3; Length 394;
Best Local Similarity 72.7%; Pred. No. 7.89e+00;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 365 fraastkktdad 375
||| ||| ||
Qy 2 FRAVITKKVAD 12

RESULT 11
ID BPL1 YEAST STANDARD; PRT; 690 AA.
AC P48435;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DE BIOTIN APO-PROTEIN LIGASE (EC 6.3.4.-).
GN BPL1 OR ACC2.
OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
FN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE; 95377607.
RA CRONAN J.E. JR., WALLACE J.C.;
RL FEMS MICROBIOL. LETT. 130:221-230(1995).
CC -!- FUNCTION: POSTTRANSLATIONAL MODIFICATION OF SPECIFIC PROTEIN BY
CC ATTACHMENT OF BIOTIN.
DR EMBL; U27182; G886081; -.
DR SGD; 10002771; BPL1.
KW LIGASE.

SQ SEQUENCE 690 AA; 76363 MW; AA6F29D3 CRC32;

Query Match 61.0%; Score 50; DB 1; Length 690;
Best Local Similarity 50.0%; Pred. No. 7.89e+00;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 679 ifksliakkv 688
l:||||:||||
Qy 1 LFRVITKKV 10

RESULT 12
ID PPS2 BACSU STANDARD; PRT; 2560 AA.
AC P39846;
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE PEPTIDE SYNTHETASE 2.
GN PPSB OR PPS2.
OS BACILLUS SUBTILIS.
OC PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
FN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA TOGNONI A., GRANDI G.;
RL SUBMITTED (JUN-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -!- COFACTOR: CONTAINS A COVALENTLY BOUND PHOSPHOPANTETHEINE
CC (POTENTIAL).
CC -!- SIMILARITY: TO OTHER ENZYMES WHICH ACT VIA AN ATP-DEPENDENT
CC COVALENT BINDING OF AMP TO THEIR SUBSTRATE.
DR EMBL; Z34883; G509469; -.
DR SUBTILIST; B610971; PPSB.
DR PROSITE; PS00012; PHOSPHOPANTETHEINE.
DR PROSITE; PS00455; AMP BINDING.
KW MULTIFUNCTIONAL ENZYME; LIGASE; REPEAT; PHOSPHOPANTETHEINE.
FT BINDING 2041 2041 PHOSPHOPANTETHEINE (POTENTIAL).
SQ SEQUENCE 2560 AA; 290161 MW; 9BAA32F6 CRC32;

Query Match 61.0%; Score 50; DB 7; Length 2560;
Best Local Similarity 41.7%; Pred. No. 7.89e+00;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 63 ifrtifikevpd 74
l:||||:|l|
Qy 1 LFRVITKKVAD 12

RESULT 13
ID UL01 HSV2H STANDARD; PRT; 224 AA.
AC P28278;
DT 01-DEC-1992 (REL. 24, CREATED)
DT 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
DT 01-DEC-1992 (REL. 24, LAST ANNOTATION UPDATE)
DE GLYCOPROTEIN 1 PRECURSOR.
GN UL1.
OS HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52).
OC VIRIDAE; DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE; ALPHAPERESVIRINAE.
FN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92113549.

RA MCGEOCH D.J., CUNNINGHAM C., MCINTYRE G., DOLAN A.;
 RL J. GEN. VIROL. 72:3057-3075(1991).
 CC -!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 ULL,
 CC HSV-2 ULL, EBV-1 62, AND VZV 60.
 DR EMBL; D10470; G221792; -.
 DR PIR; J01494; WMBEG.
 KW GLYCOPROTEIN; SIGNAL.
 FT SIGNAL 1 ? POTENTIAL.
 FT CHAIN ? 224 GLYCOPROTEIN L.
 FT CARBOHYD 170 170 POTENTIAL.
 SQ SEQUENCE 224 AA; 25192 MW; 943BCE65 CRC32;
 Query Match 59.8%; Score 49; DB 9; Length 224;
 Best Local Similarity 50.0%; Pred. No. 1.25e+01;
 Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 Db 27 vlsviakovgd 38
 Qy 1 LFRVITKQVAD 12
 RESULT 14
 ID DAPD ACTPL STANDARD; PRT; 274 AA.
 AC P41396;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE 2,3,4,5-TETRAHYDROPYRIDINE-2-CARBOXYLATE N-SUCCINYLTRANSFERASE
 DE (EC 2.3.1.117) (TETRAHYDROPICOLINATE N-SUCCINYLTRANSFERASE)
 DE (TETRAHYDROPICOLINATE SUCCINYLASE).
 GN DAPD.
 OS ACTINOBACILLUS PLEUROPNEUMONIAE (HAEMOPHILUS PLEUROPNEUMONIAE).
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
 OC PASTEURILLACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 94224145.
 RA LALONDE G., O'HANLEY P.D., STOCKER B.A., DENICH K.;
 RL MOL. MICROBIOL. 11:273-280(1994).
 CC -!- CATALYTIC ACTIVITY: SUCCINYL-COA + 2,3,4,5-TETRAHYDROPYRIDINE-
 CC 2-CARBOXYLATE = COA + N-SUCCINYL-L-2-AMINO-6-OXOHEPTANEDIOATE.
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -!- PATHWAY: FOURTH STEP IN THE BIOSYNTHESIS OF DIAMINOPIMELATE AND
 CC LYSINE FROM ASPARTATE SEMIALDEHYDE.
 CC -!- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NODL FAMILY OF
 CC ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
 DR EMBL; X63201; G38947; -.
 DR PROSITE; PS00101; HEXAPEP TRANSFERASES.
 KW DIAMINOPIMELATE BIOSYNTHESIS.
 SQ SEQUENCE 274 AA; 29761 MW; B0E49D1C CRC32;
 Query Match 59.8%; Score 49; DB 3; Length 274;
 Best Local Similarity 70.0%; Pred. No. 1.25e+01;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Db 246 lycavivkv 255
 Qy 1 LFRVITKQV 10

RESULT 15
 ID DAPD ECOLI STANDARD; PRT; 274 AA.
 AC P03948;
 DT 23-OCT-1986 (REL. 02, CREATED)
 DT 23-OCT-1986 (REL. 02, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE 2,3,4,5-TETRAHYDROPYRIDINE-2-CARBOXYLATE N-SUCCINYLTRANSFERASE
 DE (EC 2.3.1.117) (TETRAHYDROPICOLINATE N-SUCCINYLTRANSFERASE)
 DE (TETRAHYDROPICOLINATE SUCCINYLASE).
 GN DAPD.
 OS ESCHERICHIA COLI.
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
 OC ENTEROBACTERIACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 85054973.
 RA RICHAUD C., RICHAUD F., MARTIN C., HAZIZA C., PATTE J.-C.;
 RL J. BIOL. CHEM. 259:14824-14828(1984).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / W3110;
 RX MEDLINE; 94261430.
 RA FUJITA N., MORI H., YURA T., ISHIHAMA A.;
 RL NUCLEIC ACIDS RES. 22:1637-1639(1994).
 RN [3]
 RP SEQUENCE OF 1-15 FROM N.A.
 RC STRAIN=K12 / W3110;
 RX MEDLINE; 94018640.
 RA VAN HEESWIJK W.C., RABENBERG M., WESTERHOFF H.V., KAHN D.D.;
 RL MOL. MICROBIOL. 9:443-458(1993).
 RN [4]
 RP SEQUENCE OF 1-11.
 RC STRAIN=K12 / W3110;
 RA PASQUALI C., SANCHEZ J.-C., RAVIER F., GOLAZ O., HUGHES G.J.,
 RA FRUTIGER S., PAQUET N., WILKINS M., APPEL R.D., BAIRICH A.,
 RA HOCHSTRASSER D.F.;
 RL SUBMITTED (SEP-1994) TO THE SWISS-PROT DATA BANK.
 RN [5]
 RP SEQUENCE OF 1-12.
 RC STRAIN=K12 / EMG2;
 RA LINK A.J.;
 RL SUBMITTED (OCT-1994) TO THE SWISS-PROT DATA BANK.
 CC -!- CATALYTIC ACTIVITY: SUCCINYL-COA + 2,3,4,5-TETRAHYDROPYRIDINE-
 CC 2-CARBOXYLATE = COA + N-SUCCINYL-L-2-AMINO-6-OXOHEPTANEDIOATE.
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -!- PATHWAY: FOURTH STEP IN THE BIOSYNTHESIS OF DIAMINOPIMELATE AND
 CC LYSINE FROM ASPARTATE SEMIALDEHYDE.
 CC -!- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NODL FAMILY OF
 CC ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
 DR EMBL; K02970; G145712; -.
 DR EMBL; D26562; G473821; -.
 DR EMBL; Z21842; G49394; -.
 DR PIR; A00601; XNEGSD.
 DR SWISS-ZDPAGE; P03948; COLI.
 DR ECOGENE; EG10207; DAPD.
 DR PROSITE; PS00101; HEXAPEP TRANSFERASES.
 KW TRANSFERASE; ACYLTRANSFERASE; REPEAT; LYSINE BIOSYNTHESIS;
 KW DIAMINOPIMELATE BIOSYNTHESIS.

FT CONFLICT 31 31 D -> V (IN REF. 2).
 FT CONFLICT 163 163 R -> G (IN REF. 2).
 FT CONFLICT 177 177 M -> I (IN REF. 2).
 FT CONFLICT 190 190 L -> V (IN REF. 2).
 SQ SEQUENCE 274 AA; 30039 MW; CFA40D03 CRC32;

Query Match 59.8%; Score 49; DB 3; Length 274;
 Best Local Similarity 70.0%; Pred. No. 1.25e+01;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 247 lycavivkv 256
 QY 1 LFRAVITKV 10
 I: ||| |||

Search completed: Thu Apr 3 11:58:00 1997
 Job time : 8 secs.

 WVPSRFLH
 ***** (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Thu Apr 3 11:59:58 1997; MasPar time 1.74 Seconds
 Tabular output not generated. 71.041 Million cell updates/sec

Title: >US-08-190-411A-4
 Description: (1-12) from 5541104.ppt
 Perfect Score: 81
 Sequence: 1 DVKEADPTGHSY 12

Scoring table: PAM 150
 Gap 15

Searched: 88003 seqs, 10295656 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: a-geneseq25
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
 14:part14 15:part15 16:part16 17:part17 18:part18

Statistics: Mean 16.578; Variance 39.102; scale 0.424

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	81	100.0	12	15	R80620	Immunogenic peptide o	3.08e-04
2	81	100.0	309	13	R70909	Human melanoma antige	3.08e-04
3	61	75.3	9	15	R78824	MAGE-1 cytotoxic T ly	2.87e-01
4	61	75.3	9	17	R90692	Human leukocyte antige	2.87e-01
5	61	75.3	9	15	R82988	P815 antigenic peptid	2.87e-01
6	61	75.3	9	16	R83932	MHC class I restricte	2.87e-01
7	61	75.3	9	13	R65135	MAGE 1 immunogenic pe	2.87e-01
8	61	75.3	9	12	R63675	Synthetic peptide der	2.87e-01
9	61	75.3	9	15	R75954	Melanoma antigen (MAG	2.87e-01
10	61	75.3	9	9	R47330	HLA-A1 MAGE 1 antigen	2.87e-01
11	61	75.3	9	9	R49224	HLA-A1 MAGE 1 antigen	2.87e-01
12	61	75.3	9	6	R29769	Antigen E peptide.	2.87e-01
13	61	75.3	9	9	R50281	MAGE-1 nonapeptide.	2.87e-01
14	61	75.3	9	13	R65112	MAGE 1 immunogenic pe	2.87e-01
15	48	59.3	308	9	R45431	Diabetogene rad: A ty	1.80e+01
16	48	59.3	925	14	R79148	Human insulin recepto	1.80e+01
17	47	58.0	443	1	P93191	Peptide with glutamin	2.45e+01
18	46	56.8	9	9	R50287	MAGE-5 nonapeptide.	3.31e+01
19	46	56.8	9	9	R50289	MAGE-6 nonapeptide.	3.31e+01
20	46	56.8	9	9	R50288	MAGE-51 nonapeptide.	3.31e+01
21	46	56.8	999	17	R87511	Human c-mer protoonco	4.47e+01
22	45	55.6	346	10	R60653	pstS variant.	6.01e+01
23	44	54.3	77	1	P80309	Polypeptide with regi	6.01e+01
24	44	54.3	827	1	R05049	Human villin.	6.01e+01
25	43	53.1	9	15	R75942	Melanoma antigen (MAG	8.07e+01
26	43	53.1	9	16	R83931	MHC class I restricte	8.07e+01
27	43	53.1	9	9	R50284	MAGE-3 nonapeptide.	8.07e+01
28	43	53.1	9	9	R49222	HLA-A1 MAGE 3 antigen	8.07e+01
29	43	53.1	9	13	R65118	MAGE 3 immunogenic pe	8.07e+01
30	43	53.1	11	12	R73851	Antigen fragment 167,	8.07e+01
31	43	53.1	341	16	R77361	Cysteine proteinase f	8.07e+01
32	43	53.1	669	16	R86408	Human matrix metallo	8.07e+01
33	43	53.1	812	2	R10047	abaA gene of Aspergil	8.07e+01
34	43	53.1	3396	8	R43662	DEN1-S275/90 (ECACC V	8.07e+01
35	42	51.9	9	9	R50286	MAGE-41 nonapeptide.	1.08e+02
36	42	51.9	156	3	R13587	PLRV viral protein.	1.08e+02
37	42	51.9	198	16	R93137	Mouse guanylate kinas	1.08e+02
38	42	51.9	392	1	R07130	H2OB receptor.	1.08e+02
39	42	51.9	416	1	R07131	H2OA receptor.	1.08e+02
40	41	50.6	319	17	R88011	Mature Pseudomonas gl	1.44e+02
41	41	50.6	459	2	R08331	Hybrid murine IL-7 ge	1.44e+02
42	41	50.6	472	13	R67696	C. albicans caauri ke	1.44e+02
43	41	50.6	889	13	R65159	Potassium ion channel	1.44e+02
44	41	50.6	970	14	R72458	Porphyromonas gingiva	1.44e+02
45	41	50.6	1704	13	R70188	Arg-gingipain-2 prepo	1.44e+02

ALIGNMENTS

RESULT 1
 ID R80620 standard; Protein; 12 AA.

AC R80620;
 DT 28-FEB-1996 (first entry)
 DE Immunogenic peptide of tumour rejection antigen (MAGE-1).
 KW Tumour rejection antigen; MAGE-1; monoclonal antibody; MAAb;
 KW diagnosis; immunoassay; cancer; immunogen; antiserum.
 OS Homo sapiens.
 PN W09520974-A1.
 PD 10-AUG-1995.
 PF 05-JAN-1995; 000095.
 PR 01-FEB-1994; US-190411.
 PA (LUDW-) LUDWIG INST CANCER RES.
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 PA (SLOK) MEMORIAL SLOAN-KETTERING CANCER CENT.
 PI Boon-falleur T, Chen Y, Garin-chesa P, Old LJ, Rettig WJ;
 PI Stockert E, Van der bruggen P;
 DR WPI; 95-283606/37.
 DT New monoclonal antibody binding specifically to MAGE-1 - useful for
 PT diagnosis and monitoring of cancer, also new hybridomas, recombinant
 PT MAGE-1 and immunogenic peptide(s)
 PT Claim 12; Page 20; 33pp; English.
 PS A monoclonal antibody directed against the tumour rejection antigen
 CC (MAGE-1) can be used to detect MAGE-1 in samples by standard
 CC immunoassay methods for diagnosis and monitoring of cancer etc. The
 CC monoclonal antibody is designated MA454 and is produced by the
 CC hybridoma deposited as ATCC HB11540. The monoclonal antibody is
 CC specific for MAGE-1, having no reactivity for MAGE-2 or MAGE-3.
 CC Peptide fragments of MAGE-1 (See R80618-20) may be useful as
 CC immunogens for production of the monoclonal antibody and antiserum.
 SQ Sequence 12 AA;

Query Match 100.0%; Score 81; DB 15; Length 12;
 Best Local Similarity 100.0%; Pred. No. 3.08e-04; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 0;
 Db 1 dvkeadptghsy 12
 QY 1 DVKEADPTGHSY 12

RESULT 2
 ID R70909 standard; Protein; 309 AA.
 AC R70909;
 DT 09-OCT-1995 (first entry)
 DE Human melanoma antigen MAGE-1.
 KW Human melanoma antigen; MAGE-1; vaccines; MAGE associated tumours;
 KW HLA-restricted cytotoxic T-lymphocyte activity.
 OS Homo sapiens.
 PN W09504542-A.
 PD 16-FEB-1995.
 PF 02-AUG-1994; D08721.
 PR 06-AUG-1993; US-103623.
 PA (CYTE-) CYTEL CORP.
 PI Fikes JD, Livingston BD, Sette AD, Sidney JC;
 DR WPI; 95-090881/12.
 DT N-PSDB; Q85435.
 PT Human melanoma antigen, MAGE-1, peptide(s) - useful for
 PT stimulating immune response against melanoma
 PS Example 1; Fig 1; 59pp; English.
 CC Q85435 encodes R70909 human melanoma antigen MAGE-1, it was used
 CC to produce the C-terminal MAGE-1 peptides described in R70915 to

CC R70969. These peptides are useful for defining epitopes that
 CC engender a HLA-restricted cytotoxic lymphocyte activity against
 CC MAGE-1 antigens. Compsns. containing these peptides can be
 CC administered, as a vaccine to patients susceptible to MAGE
 CC associated tumours, e.g. melanomas.
 SQ Sequence 309 AA;

Query Match 100.0%; Score 81; DB 13; Length 309;
 Best Local Similarity 100.0%; Pred. No. 3.08e-04;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 158 dvkeadptghsy 169
 QY 1 DVKEADPTGHSY 12

RESULT 3
 ID R78824 standard; peptide; 9 AA.
 AC R78824;
 DT 26-MAR-1996 (first entry)
 DE MAGE-1 cytotoxic T lymphocyte epitope.
 KW MAGE-1; cytotoxic T; CTL; epitope; helper T; HTL; lymphocyte;
 KW cell; viruses; parasites; tumours; antigens; disease prevention;
 KW treatment.
 OS Homo sapiens.
 PN W09522317-A1.
 PD 24-AUG-1995.
 PF 16-FEB-1995; U02121.
 PR 16-FEB-1994; US-197484.
 PA (CYTE-) CYTEL CORP.
 PI Cellis E, Chesnut RW, Grey H, Sette AD, Vitiello MA;
 DR WPI; 95-302545/39.
 DT Compn. inducing cytotoxic T lymphocyte response to pref. viral,
 PT bacterial, parasitic or tumour antigens - useful in the treatment
 PT and prevention of diseases associated with the antigen e.g.
 PT hepatitis B
 PS Disclosure; Page 17; 109pp; English.
 CC A compsn. which induces a cytotoxic T lymphocyte (CTL) response to
 CC an antigen (Ag) in a mammal comprises, a CTL Ag response inducing
 CC peptide (i.e. R78824-R78853) and a lipid conjugated helper T cell
 CC inducing peptide. The compsn. induces a CTL response to bacterial,
 CC viral or tumour Ags, and is therefore useful in the treatment and
 CC prevention of diseases associated with the Ag.
 SQ Sequence 9 AA;

Query Match 75.3%; Score 61; DB 15; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.87e-01;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 eadptghsy 9
 QY 4 EADPTGHSY 12

RESULT 4
 ID R90692 standard; peptide; 9 AA.
 AC R90692;
 DT 31-JUL-1996 (first entry)
 DE Human leukocyte antigen (HLA-A1) presented peptide M22-E.
 KW Human leukocyte antigen; HLA-A1; MAGE-1 derived;

KW blood mononuclear cell; BMC; CD8-beta+ cell; cytolytic T cell;
KW CTL cell; treatment; tumour cell; diagnosis; assay;
KW presented peptide.
OS Synthetic.
PN WO9535500-A1.
PD 28-DEC-1995.
PF 14-JUN-1995; U07559.
PR 17-JUN-1994; US-261541.
PA (LUDW-) LUDWIG INST CANCER RES.
PI Boon-Falleur T, Coulie P, Van Der Bruggen P;
DR WPI; 96-058510/06.
PT Prod'n. of specific cytolytic T cell sub-populations - by contacting
PT blood mononuclear cells with specific peptide(s) and a population of
PT CD8-beta(+) cells
PS Claim 5; Page 19; 25pp; English.
CC The present peptide is the human leukocyte antigen (HLA-A1), MAGE-1
CC derived presented peptide, MZ2-E. By contacting a sample of blood
CC mononuclear cells (BMC) with the peptide (which binds directly to
CC HLA-A1 mols. on the surface of the BMC) and CD8-beta+ cells (which
CC stimulate peptide/HLA-A1 complex specific CD8-beta+ cells), a
CC peptide/HLA-A1 complex specific cytolytic T (CTL) cell
CC subpopulation can be obt'd.. The CTL cells obt'd. can be
CC administered to a patient to treat tumour cell related conditions,
CC and can be used in diagnostic methods, e.g. in assays for the
CC peptide/HLA-A1 complex.
SQ Sequence 9 AA;

Query Match 75.3%; Score 61; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.87e-01;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 eadptghsy 9
| | | | |
Qy 4 EADPTGHSY 12

RESULT 5
ID R62988 standard; Peptide; 9 AA.
AC R62988;
DT 26-FEB-1996 (first entry)
DE P815 antigenic peptide.
KW P815 antigen; P1A antigen; cancer; vaccine.
OS Synthetic.
PN WO9523874-A1.
PD 08-SEP-1995.
PF 23-FEB-1995; U02203.
PR 01-MAR-1994; US-204727.
PR 10-MAR-1994; US-209172.
PR 01-SEP-1994; US-299849.
PR 30-NOV-1994; US-346774.
PA (LUDW-) LUDWIG INST CANCER RES.
PI Boon-Falleur T, Brasseur F, Chomez P, De Plaen E;
PI De Smet C, Gaugler B, Lethe B, Marchand M, Patard J;
PI Szikora J, Van Den Eynde B, Van Derbruggen P, Weynants P;
DR WPI; 95-320366/41.
PT Determin. of cancerous condition(s) - using a nucleic acid as a
PT primer to determine expression of a MAGE tumour rejection antigen
PT precursor
PS Example 13; Page 22; 121pp; English.
CC Using the sequence of the P815A antigen precursor gene P1A

CC (T01176), an antigenic peptide (R82988) which was A+B+ (i.e.
CC characteristic of cells which express both A and B antigens) was
CC produced. The peptide lysed PO.HTR cells in the presence of
CC cytolytic T lymphocyte cell lines, and may be useful as a vaccine
CC component.
SQ Sequence 9 AA;

Query Match 75.3%; Score 61; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.87e-01;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 eadptghsy 9
| | | | |
Qy 4 EADPTGHSY 12

RESULT 6
ID R83932 standard; peptide; 9 AA.
AC R83932;
DT 05-JUN-1996 (first entry)
DE MHC class I restricted antigenic peptide #2.
KW MHC class I; antigen; MAGE; melanoma; breast cancer; bladder cancer;
KW Titermax; cytotoxic T-lymphocyte; tumour; pathogenic disease; bacteria;
KW parasite; human; animal.
OS Synthetic.
PN WO9528958-A1.
PD 02-NOV-1995.
PF 21-APR-1995; U04975.
PR 22-APR-1994; US-233496.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
PI Dyllal R, Nikolic-Zugic J;
DR WPI; 95-382848/49.
PT Cytotoxic T-cell induction by MHC class I-restricted peptide in
PT adjuvant - useful for treating tumours and bacterial or parasitic
PT pathogenic diseases
PS Claim 11; Page 38; 50pp; English.
CC The sequences given in R83931-49 are MHC class I restricted 8-12
CC amino acid antigenic peptides. This peptide is derived from MAGE
CC and is present in melanoma, breast and bladder cancer. These
CC peptides may be administered to a subject in combination with a
CC suitable adjuvant, pref. Titermax (RIM), to induce cytotoxic T-
CC lymphocytes. This method may be used in the treatment of a tumour
CC or a pathogenic disease, esp. diseases of bacterial or parasitic
CC origin, in humans and animals, e.g. monkeys, dogs cows, horses, etc.
SQ Sequence 9 AA;

Query Match 75.3%; Score 61; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.87e-01;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 eadptghsy 9
| | | | |
Qy 4 EADPTGHSY 12

RESULT 7
ID R65135 standard; peptide; 9 AA.
AC R65135;
DT 09-OCT-1995 (first entry)
DE MAGE 1 immunogenic peptide A01.

KW MAGE 1; immunogenic peptide A01; cytotoxic C cells;
KW in vitro activation; cancer; AIDS; bacterial infections; malaria;
KW fungal infections; tuberculosis; hepatitis.
OS Homo sapiens.
PN W09504817-A.
PD 16-FEB-1995.
PF 01-AUG-1994; U08672.
PR 06-AUG-1993; US-103401.
PA (CYTE-) CYTEL CORP.
PI Celis E, Kubo R, Seria H, Tsai V, Wentworth P;
DR WPI; 95-090895/12.
PT In vitro activation of cytotoxic T cells for selected killing of
PT target cells - for treating e.g. cancer, AIDS, hepatitis etc.by
PT incubating them with antigen presenting cells loaded with
PT appropriate immunogenic peptide
PS Example 3; Page 38; 53pp; English.
CC R65109-R65145 are immunogenic peptides, they are used in a new
CC method for the in vitro activation of cytotoxic T cells (CTC).
CC This is achieved by incubating the CTCs with antigen presenting
CC cells loaded with an appropriate immunogenic peptide (e.g. one
CC of the above peptides). By selecting the peptides used the
CC following diseases and infections can be treated; cancer, AIDS,
CC hepatitis, other viral and bacterial infections, malaria and
CC tuberculosis.
CC Sequence 9 AA;

Query Match 75.3%; Score 61; DB 13; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.87e-01;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 eadptghsy 9
|||||
Qy 4 EADPTGHSY 12

RESULT 8
ID R63675 standard; Protein; 9 AA.
AC R63675;
DT 22-JUN-1995 (first entry)
DE Synthetic peptide derived from exon 3.1 of MAGE 1.
KW Melanoma antigen-1; MAGE-1; cytolytic T cells; antigen E; exon 3.1.
OS Synthetic.
PN W09423031-A.
PD 13-OCT-1994.
PF 17-MAR-1994; US-037230.
PR 26-MAR-1993; US-037230.
PA (LUDW-) LUDWIG INST CANCER RES.
PI Boon-fallieur T, Gaugler B, Van DEN EYNDE B, Van DER BRUGGEN P;
DR WPI; 94-333192/41.
PT New tumour rejection antigen precursor MAGE3 - useful in
PT treatment and diagnosis of cancer
PS Example 34; Page 36; 105pp; English.
CC R63675 is a synthetic peptide derived from exon 3.1 of melanoma
CC antigen-1 (MAGE-1), it was used to transfer antigen-E cytolytic T
CC lymphocyte sensitivity to normally non-sensitive cells.
CC Sequence 9 AA;

Query Match 75.3%; Score 61; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.87e-01;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 eadptghsy 9
|||||
Qy 4 EADPTGHSY 12

RESULT 9
ID R75954 standard; Peptide; 9 AA.
AC R75954;
DT 06-MAR-1996 (first entry)
DE Melanoma antigen (MAGE-1) epitope.
KW MAGE-3; melanoma antigen; vaccine; immune response; immunogenic peptide;
KW cytotoxic T lymphocyte response; CTL; melanoma; breast cancer; antibody.
OS Homo sapiens.
PN W09519783-A1.
PD 27-JUL-1995.
PF 25-JAN-1995; U01000.
PR 25-JAN-1994; US-186266.
PA (CYTE-) CYTEL CORP.
PI Celis E, Grey EM, Kubo RT, Sette A;
DR WPI; 95-269270/35.
PT Immunogenic peptide(s) that induce immune response to cancer cells
PT - that express a MAGE-3 protein peptide epitope used in vaccines or
PT adoptive immunotherapy to induce cytotoxic T lymphocytes
PS Example; Page 33; 44pp; English.
CC R75954 is derived from MAGE-1 protein. It was used to show the
CC specificity of CTL response to MAGE-3 peptides shown in R75942-53.
CC R75942 is derived from the sequence of the melanoma antigen (MAGE-3)
CC protein and can be used to elicit a primary cytotoxic T lymphocyte
CC response against cells expressing MAGE-3. Synthetic peptides R75945-53
CC can be used therapeutically to elicit CTL responses to melanoma, breast,
CC colon, prostate, or other cells which express proteins with this epitope.
CC The peptides have specific HLA-A1 binding capacity.
CC Sequence 9 AA;

Query Match 75.3%; Score 61; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.87e-01;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 eadptghsy 9
|||||
Qy 4 EADPTGHSY 12

RESULT 10
ID R47330 standard; Protein; 9 AA.
AC R47330;
DT 31-AUG-1994 (first entry)
DE HLA-A1 MAGE 1 antigen peptide fragment 161-169.
KW Immunogenic; HLA-A3.2; HLA-A1; HLA-A11; binding motif; MHC molecule;
KW immune response; viral infection; cancer; prostate cancer; lymphoma;
KW hepatitis; AIDS; antibody; diagnosis; melanoma antigen.
OS Synthetic.
PN W09403205-A.
PD 17-FEB-1994.
PF 06-AUG-1993; U07421.
PR 07-AUG-1992; US-926666.
PR 05-MAR-1993; US-027746.
PA (CYTE-) CYTEL CORP.
PI Celis E, Grey EM, Kubo RT, Sette A;

WPI; 94-065403/08.
PT Peptide which specifically binds selected MHC allele - used to
PT induce an immune response for treatment or prevention of viral
PT infection or cancer, or for diagnosis
PS Example 8; Page 52; 150pp; English.
CC The sequences given in R47304-33 and R49201-44 are immunogenic
CC peptides which have a HLA-A3.2, HLA-A1 or a HLA-A11 binding motif.
CC These peptides may be used in the composition of the invention.
CC These peptides are capable of binding selected MHC molecules and
CC inducing an immune response. They can be used to treat and/or
CC prevent viral infection and cancer, eg. prostate cancer, lymphoma,
CC hepatitis or AIDS. They can also be used to produce antibodies for
CC use as diagnostic or therapeutic agents. The peptides can also be
CC used as diagnostic agents.
SQ Sequence 9 AA;

Query Match 75.3%; Score 61; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.87e-01;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 eadptghsy 9
| | | | | | | |
QY 4 EADPTGHSY 12

RESULT 11
ID R49224 standard; Protein; 9 AA.
AC R49224;
DT 31-AUG-1994 (first entry)
DE HLA-A1 MAGE 1 antigen peptide fragment 958.01.
KW Immunogenic; HLA-A3.2; HLA-A1; binding motif; MHC molecule;
KW immune response; viral infection; cancer; prostate cancer; lymphoma;
KW hepatitis; AIDS; antibody; diagnosis; melanoma antigen.
OS Synthetic.
PN W09403205-A.
PD 17-FEB-1994.
PF 06-AUG-1993; U07421.
PR 07-AUG-1992; US-928666.
PR 05-MAR-1993; US-027746.
PA (CYTE-) CYTEL CORP.
PI Celis E, Grey HM, Kubo RT, Sette A;
DR WPI; 94-065403/08.
PT Peptide which specifically binds selected MHC allele - used to
PT induce an immune response for treatment or prevention of viral
PT infection or cancer, or for diagnosis
PS Example 16; Page 116; 150pp; English.
CC The sequences given in R47304-33 and R49201-44 are immunogenic
CC peptides which have a HLA-A3.2, HLA-A1 or a HLA-A11 binding motif.
CC These peptides may be used in the composition of the invention.
CC These peptides are capable of binding selected MHC molecules and
CC inducing an immune response. They can be used to treat and/or
CC prevent viral infection and cancer, eg. prostate cancer, lymphoma,
CC hepatitis or AIDS. They can also be used to produce antibodies for
CC use as diagnostic or therapeutic agents. The peptides can also be
CC used as diagnostic agents.
SQ Sequence 9 AA;

Query Match 75.3%; Score 61; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.87e-01;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 eadptghsy 9
| | | | | | | |
QY 4 EADPTGHSY 12

RESULT 12
ID R29769 standard; Peptide; 9 AA.
AC R29769;
DT 22-APR-1993 (first entry)
DE Antigen E peptide.
KW Antigen; tumorigenic cell; A+ B+; T-cell; response; syngeneic;
KW animal; mouse; tumour rejection antigen precursor; TRAP; PLA.
OS Homo sapiens.
PN W09220356-A.
PD 26-NOV-1992.
PF 22-MAY-1992; U04354.
PR 23-MAY-1991; US-705702.
PR 09-JUL-1991; US-728838.
PR 23-SEP-1991; US-764364.
PR 12-DEC-1991; US-807043.
PA (LUDW-) LUDWIG INST CANCER RES.
PI Boon T, Chomez P, De Plaen E, Lurquin C, Traversari C;
PI Van Den Eynde B, Van Der Bruggen P, Van Pel A;
DR WPI; 92-415460/50.
PT Nucleic acid mol. encoding a human tumour rejection antigen
PT precursor - useful as an immunostimulant in a vaccine for
PT treating and preventing cancers, also useful in diagnosis
PS Disclosure; Page 97; 142pp; English.
CC This sequence represents the sequence of the antigen E. Antigens such
CC as this one cause a T-cell response to be elicited which transplanted
CC into a syngeneic animal, usually a mouse. This antigen is derived from
CC the cell line MEL3.1. See also Q32351.
SQ Sequence 9 AA;

Query Match 75.3%; Score 61; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.87e-01;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 eadptghsy 9
| | | | | | | |
QY 4 EADPTGHSY 12

RESULT 13
ID R50281 standard; Protein; 9 AA.
AC R50281;
DT 26-SEP-1994 (first entry)
DE MAGE-1 nonapeptide.
KW MAGE; nonapeptide; cancer; melanoma; breast cancer; HLA;
KW histocompatibility; human leucocyte antigen; probe; treatment;
KW therapy; vaccine.
OS Synthetic.
PN W09405304-A.
PD 17-MAR-1994.
PF 30-AUG-1993; U08157.
PR 31-AUG-1992; US-938334.
PR 26-MAR-1993; US-037230.
PR 07-JUN-1993; US-073103.
PA (LUDW-) LUDWIG INST CANCER RES.

PI Boon-falleur T, De Plaen E, Lurquin C, Traversari C;
 DR Van Derbruggen P;
 DR WPI; 94-100844/12.
 DR N-PSDB; Q44751.
 PT New nona:peptide derived from tumour rejection antigen precursor
 PT - presented by HLA-A1 cancer cells, for use in diagnosis or
 PT therapy of esp. melanoma and breast cancer.
 PS Disclosure; Page 19; 33pp; English.
 CC An isolated nonapeptide having the amino acid sequence Glu-Val-Asp-
 CC Pro-Ile-Gly-His-Leu-Iyr is derived from the tumour rejection antigen
 CC precursor encoded by the MAGE-3 gene and presented by HLA-A1. The
 CC nonapeptide can be used in a vaccine to treat a cancerous condition
 CC involving HLA-A1 subtype cancerous cells. The nucleic acid encoding
 CC the nonapeptide can be used as a probe to identify tumour cells.
 CC This sequence is homologous to the peptide described and is encoded
 CC by the MAGE-1 gene.
 SQ Sequence 9 AA;

Query Match 75.3%; Score 61; DB 9; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.87e-01; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0;

Db 1 eadptghsy 9
 |||||
 QY 4 EADPTGHSY 12

RESULT 14
 ID R65112 standard; peptide; 9 AA.
 AC R65112;
 DT 06-OCT-1995 (first entry)
 DE MAGE 1 immunogenic peptide 161-169.
 KW MAGE 1; immunogenic peptide 161-169; cytotoxic C cells;
 KW in vitro activation; cancer; AIDS; bacterial infections; malaria;
 KW fungal infections; tuberculosis; hepatitis.
 OS Homo sapiens.
 PN W09504817-A.
 FD 16-FEB-1995.
 FF 01-AUG-1994; 008672.
 PR 06-AUG-1993; US-103401.
 PA (CYTE-) CYTEL CORP.
 PI Celis E, Kubo R, Serrà H, Tsai V, Wentworth P;
 DR WPI; 95-090895/12.
 PT In vitro activation of cytotoxic T cells for selected killing of
 PT target cells - for treating e.g. cancer, AIDS, hepatitis etc.by
 PT incubating them with antigen presenting cells loaded with
 PT appropriate immunogenic peptide
 PS Example 3; Page 35; 53pp; English.
 CC R65109-R65145 are immunogenic peptides, they are used in a new
 CC method for the in vitro activation of cytotoxic T cells (CTC).
 CC This is achieved by incubating the CTCs with antigen presenting
 CC cells loaded with an appropriate immunogenic peptide (e.g. one
 CC of the above peptides). By selecting the peptides used the
 CC following diseases and infections can be treated; cancer, AIDS,
 CC hepatitis, other viral and bacterial infections, malaria and
 CC tuberculosis.
 SQ Sequence 9 AA;

Query Match 75.3%; Score 61; DB 13; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.87e-01;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 eadptghsy 9
 |||||
 QY 4 EADPTGHSY 12

RESULT 15
 ID R45431 standard; Protein; 308 AA.
 AC R45431;
 DT 13-JUN-1994 (first entry)
 DE Diabetogene rad; A type II.
 KW Diabetogene rad; rad gene; diabetogene rad protein; diabetes;
 KW obesity.
 OS Homo sapiens.
 PN W09400558-A.
 PD 06-JAN-1994.
 PR 11-JUN-1993; U05643.
 PR 19-JUN-1992; US-901710.
 PA (JOSL-) JOSLIN DIABETES CENT INC.
 PI Kahn CR, Reynet C;
 DR WPI; 94-026198/03.
 DR P-PSDB; Q55175.
 PT Purified DNA - includes type II diabetes-specific gene,
 PT Diabetogenic rad
 PS Disclosure; Page 37-38; 57pp; English.
 CC A gene encoding diabetogene rad protein R45431 is given in sequence
 CC Q55175. The gene is used to determine the risk of diabetes or
 CC obesity, and the protein is used to treat deficiency of diabetogene
 CC product.
 SQ Sequence 308 AA;

Query Match 59.3%; Score 48; DB 9; Length 308;
 Best Local Similarity 55.6%; Pred. No. 1.80e+01;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 119 eaeaaghty 127
 ||::|||
 QY 4 EADPTGHSY 12

Search completed: Thu Apr 3 12:00:05 1997
 Job time : 7 secs.

 WIPESHI (TM)

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Apr 3 11:59:33 1997; MspPar time 2.35 Seconds
131.633 Million cell updates/sec
Tabular output not generated.

Title: >US-08-190-411A-4
Description: (1-12) from 5541104.pap
Perfect Score: 81
Sequence: 1 DVKEADPTGHSY 12

Scoring table: PAM 150
Gap 15

Searched: 82182 seqs, 25727515 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir48
1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4
8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unann
14:unrev

Statistics: Mean 22.546; Variance 27.701; scale 0.814

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description	Pred. No.
1	81	100.0	280	12	JC2358 tumor-associated ant	9.68e-08
2	62	76.5	317	12	JC2359 tumor-associated ant	5.43e-03
3	57	70.4	347	11	138008 MAGE-Xp protein - hu	7.72e-02
4	57	70.4	347	11	S52167 MAGE-Xp protein - hu	7.72e-02
5	53	65.4	314	12	JC2360 tumor-associated ant	5.90e-01
6	52	64.2	417	4	S16582 fructose-bisphosphat	9.69e-01
7	50	61.7	314	12	JC2361 tumor-associated ant	2.56e+00
8	50	61.7	381	9	S29560 fructose-bisphosphat	2.56e+00
9	50	61.7	835	7	A49891 outer membrane prote	2.56e+00
10	49	60.5	417	4	A43929 carboxypeptidase A (4.13e+00
11	49	60.5	3898	3	A44217 genome polypeptidase	4.13e+00
12	48	59.3	150	11	S55370 RNA polymerase II ch	6.60e+00
13	48	59.3	269	11	A49334 Ras homolog Rad - hu	6.60e+00
14	48	59.3	925	11	A39216 nucleotide pyrophosph	6.60e+00
15	47	58.0	197	1	KIPGGU guanylate kinase (EC	1.05e+01
16	47	58.0	199	14	S32545 Guanylate kinase - p	1.05e+01
17	47	58.0	444	2	AJBSOU glutamate--ammonia	1.05e+01
18	47	58.0	444	2	AJBSOS glutamate--ammonia	1.05e+01
19	47	58.0	445	4	A48947 glutamate--ammonia	1.05e+01
20	47	58.0	497	6	S33938 penton protein (III)	1.05e+01
21	47	58.0	633	11	A36353 DNA repair protein X	1.05e+01
22	46	56.8	9	11	PH1301 MAGE 6 protein - hum	1.66e+01
23	46	56.8	9	11	PH1300 MAGE 51 protein - hu	1.66e+01
24	46	56.8	9	11	PH1299 MAGE 5 protein - hum	1.66e+01
25	46	56.8	147	1	PSKFA4 phospholipase A2 (EC	1.66e+01

26	46	56.8	439	9	S25483 ribulose-bisphosphat	1.66e+01
27	46	56.8	543	10	S59294 probable transcripti	1.66e+01
28	46	56.8	583	1	A25937 arsenical pump-drivi	1.66e+01
29	45	55.6	125	8	D49923 ribosomal protein S1	2.60e+01
30	45	55.6	581	6	S04857 penicillin-binding p	2.60e+01
31	45	55.6	581	6	S00916 penicillin-binding p	2.60e+01
32	45	55.6	582	7	S49090 penicillin-binding p	2.60e+01
33	45	55.6	725	11	A45033 myelin transcription	2.60e+01
34	45	55.6	1033	7	S02168 type I site-specific	2.60e+01
35	44	54.3	22	8	D37145 hypothetical hlv pro	4.04e+01
36	44	54.3	222	8	S39681 hypothetical protein	4.04e+01
37	44	54.3	261	9	S32899 14-3-3 brain protein	4.04e+01
38	44	54.3	377	8	S52537 emm L 15 protein - S	4.04e+01
39	44	54.3	438	6	S55631 virion protein kinase	4.04e+01
40	44	54.3	469	2	AJZRQL glutamate--ammonia	1.66e+01
41	44	54.3	488	11	S55874 sulfite oxidase (EC	4.04e+01
42	44	54.3	539	8	D36904 carbon dioxide conce	4.04e+01
43	44	54.3	629	10	S4567 hypothetical protein	4.04e+01
44	44	54.3	789	9	S46631 aconitate hydratase	4.04e+01
45	44	54.3	827	2	A31642 villin - human	4.04e+01

ALIGNMENTS

RESULT 1

ENTRY JC2358 #type complete
TITLE tumor-associated antigen, MAGE-1 - human
ORGANISM #formal name Homo sapiens #common name man
DATE 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 15-Mar-1996

ACCESSIONS JC2358
REFERENCE JC2358
#authors Ding, M.; Beck, R.J.; Keller, C.J.; Fenton, R.G.
#journal Biochem. Biophys. Res. Commun. (1994) 202:549-555
#title Cloning and analysis of MAGE-1-related genes.
#accession JC2358

GENETICS #molecule type mRNA
#residues 1-280 #label DIN
#experimental_source melanoma cell line DM150

FEATURE MAGE
#region HLA-A1 binding #status predicted
161-169 #length 280 #molecular-weight 30932 #checksum 467

SUMMARY

Query Match 100.0%; Score 81; DB 12; Length 280;
Best Local Similarity 100.0%; Pred. No. 9.68e-08;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 158 dvkeadptghsy 169
|||||
QY 1 DVKEADPTGHSY 12

RESULT 2

ENTRY JC2359 #type complete
TITLE tumor-associated antigen, MAGE-X2 - human
ORGANISM #formal name Homo sapiens #common name man
DATE 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 15-Mar-1996

```

JC2359
JC2358
#authors Ding, M.; Beck, R.J.; Keller, C.J.; Fenton, R.G.
#journal Biochem. Biophys. Res. Commun. (1994) 202:549-555
#title Cloning and analysis of WAGE-1-related genes.
#accession JC2359
#molecule_type mRNA
#residues 1-317 #label DIN
#experimental_source melanoma cell line DM150
GENETICS
#gene MAGE-X2
FEATURE
169-177 #region HLA-A1 binding #status predicted
SUMMARY
#length 317 #molecular-weight 34928 #checksum 9004
Query Match 76.5%; Score 62; DB 12; Length 317;
Best local similarity 66.7%; Pred. No. 5.43e-03;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Db 166 dvkedpstsnty 177
||||| |||:::|
QY 1 DVKEADPTGHSY 12
RESULT 3
ENTRY #type complete
TITLE MAGE-Xp protein - human
ORGANISM #formal name Homo sapiens #common name man
DATE 01-Mar-1996 #sequence_revision 01-Mar-1996 #text_change
01-Mar-1996
ACCESSIONS I38008
REFERENCE I38008
#authors Muscatelli, F.; Walker, A.P.; De Plaen, E.; Stafford, A.N.; Monaco, A.P.
#journal Proc. Natl. Acad. Sci. U.S.A. (1995) 92:4987-4991
#title Isolation and characterization of a WAGE gene family in the Xp21.3 region.
#cross-references MUID:95281581
#accession I38008
#status preliminary
#molecule_type mRNA
#residues_ 1-347 #label RES
#cross-references EMBL:X82539; NID:g608992; CDS_PID:g608993
GENETICS
#gene GDB:MAGE11-LSB
#cross-references GDB:G00-635-712
#map_position Xp21.3
#note gene name MAGE-Xp
SUMMARY
#length 347 #molecular-weight 39152 #checksum 8233
Query Match 70.4%; Score 57; DB 11; Length 347;
Best local similarity 50.0%; Pred. No. 7.72e-02;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
Db 164 dlkednpsshty 175
||||| |||:::|
QY 1 DVKEADPTGHSY 12
RESULT 4

```

ENTRY	S52167	#type complete	
TITLE	MAGE-Xp protein - human		
ORGANISM	#formal name Homo sapiens	#common name man	
DATE	07-May-1995	#sequence_revision 21-Jul-1995	#text_change
ACCESSIONS	S52167		
REFERENCE	Muscatelli, F.; Walker, A.P.; de Plaen, E.; Stafford, A.N.; Monaco, A.P.		
#authors			
#submission	submitted to the EMBL Data Library, November 1994		
#description	Isolation and characterization of a new MAGE gene family in the Xp21.3 region.		
#accession	S52167		
#status	preliminary		
#molecule_type	mRNA		
#residues	1-347	#label MUS	
#cross-references	EMBL:X82539		
SUMMARY	#length 347 #molecular-weight 39152 #checksum 8233		
Query Match	70.4%;	Score 57; DB 11; Length 347;	
Best Local Similarity	50.0%;	Pred. No. 7.72e-02;	
Matches	6; Conservative	5; Mismatches 1; Indels 0; Gaps 0;	
Db	164 dikednpsshty 175		
QY	1 DVKEADPTGHSY 12		
RESULT	5		
ENTRY	JC2360	#type complete	
TITLE	tumor-associated antigen , MAGE-3b - human		
ORGANISM	#formal name Homo sapiens	#common name man	
DATE	20-Feb-1995	#sequence_revision 20-Feb-1995	#text_change
ACCESSIONS	JC2360		
REFERENCE	JC2358		
#authors	Ding, M.; Beck, R.J.; Keller, C.J.; Fenton, R.G.		
#journal	Biochem. Biophys. Res. Commun. (1994) 202:549-555		
#title	Cloning and analysis of MAGE-1-related genes.		
#accession	JC2360		
#molecule_type	mRNA		
#residues	1-314	#label DIN	
#experimental_source	melanoma cell line DM150		
GENETICS			
#gene	MAGE-3b		
FEATURE			
168-176			
SUMMARY	#region HLA-A1 binding #status predicted		
	#length 314 #molecular-weight 34891 #checksum 9870		
Query Match	65.4%;	Score 53; DB 12; Length 314;	
Best Local Similarity	50.0%;	Pred. No. 5.90e-01;	
Matches	6; Conservative	3; Mismatches 3; Indels 0; Gaps 0;	
Db	165 elmevdpighvy 176		
QY	1 DVKEADPTGHSY 12		
RESULT	6		
ENTRY	S16582	#type complete	

```

TITLE      fructose-bisphosphatase (EC 3.1.3.11) precursor, chloroplast
ORGANISM   - Arabidopsis thaliana
            #formal_name Arabidopsis thaliana #common_name mouse-ear
            cress
DATE       21-Nov-1993 #sequence_revision 12-May-1995 #text_change
            12-May-1995
ACCESSIONS S16582
REFERENCE   Hornebell, P.R.; Raines, C.A.
            Plant Mol. Biol. (1991) 17:185-186
            Nucleotide sequence of a cDNA clone encoding chloroplast
            fructose-1,6-bisphosphatase from Arabidopsis thaliana.
            #cross-references MIM:91329733
            #accession S16582
            #molecule_type mRNA
            #residues 1-417 #label HOR
            #cross-references EMBL:X58148
            #experimental_source clone AFBP1
GENETICS   nuclear
            #superfamily fructose-bisphosphatase
CLASSIFICATION
KEYWORDS   Calvin cycle; chloroplast; gluconeogenesis; phosphoric
            monoester hydrolase
FEATURE    1-58
            #domain transit peptide (chloroplast) #status predicted
            #label TNP\
59-417     #product fructose-bisphosphatase #status predicted
            #label MAT
SUMMARY    #length 417 #molecular-weight 45177 #checksum 7441

Query Match      64.2%; Score 52; DB 4; Length 417;
Best Local Similarity 50.0%; Pred. No. 9.69e-01;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 314 dlkdpptgkpy 325
   1:::||||:
Qy 1 DVKEADPTGHSY 12

RESULT 7
ENTRY   JC2361 #type complete
TITLE   tumor-associated antigen, MAGE-3 - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE     20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
            15-Mar-1996
ACCESSIONS JC2361
REFERENCE   JC2358
            Ding, M.; Beck, R.J.; Keller, C.J.; Fenton, R.G.
            Biochem. Biophys. Res. Commun. (1994) 202:549-555
            Cloning and analysis of MAGE-1-related genes.
            #accession JC2361
            #molecule_type mRNA
            #residues 1-314 #label DIN
            #experimental_source melanoma cell line DM150
GENETICS   MAGE-3
            #region HLA-A1 binding #status predicted
FEATURE    168-176
            #length 314 #molecular-weight 34747 #checksum 1621
SUMMARY

```

```

Query Match      61.7%; Score 50; DB 12; Length 314;
Best Local Similarity 50.0%; Pred. No. 2.56e+00;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 165 elmevdipghly 176
   :::| |||
Qy 1 DVKEADPTGHSY 12

RESULT 8
ENTRY   S29560 #type fragment
TITLE   fructose-bisphosphatase (EC 3.1.3.11) - garden pea (fragment)
ORGANISM #formal_name Pisum sativum #common_name garden pea
DATE     22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
            10-Nov-1995
ACCESSIONS S29560
REFERENCE   Carrasco, J.L.; Chueca, A.; Hermoso, R.; Lazaro, J.J.; Ramos,
            J.L.; Sahrawy, M.; Prado, F.; Lopez Gorge, J.
            Submitted to the EMBL Data Library, October 1992
            Cloning, structure and expression of a pea cDNA clone coding
            for a photosynthetic FBPase with different features from
            those of the leaf chloroplastic enzyme.
            #accession S29560
            #molecule_type mRNA
            #residues 1-381 #label CAR
            #cross-references EMBL:X68826
            phosphoric monoester hydrolase
            #length 381 #checksum 9664
SUMMARY

Query Match      61.7%; Score 50; DB 9; Length 381;
Best Local Similarity 50.0%; Pred. No. 2.56e+00;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 278 dlkepgsgkpy 289
   1:::|:|:|
Qy 1 DVKEADPTGHSY 12

RESULT 9
ENTRY   A49891 #type complete
TITLE   outer membrane protein FasD precursor - Escherichia coli
ORGANISM #formal_name Escherichia coli
DATE     11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change
            11-Aug-1995
ACCESSIONS A49891
REFERENCE   A49891
            Schifferli, D.M.; Alrutiz, M.A.
            J. Bacteriol. (1994) 176:1099-1110
            Permissive linker insertion sites in the outer membrane
            protein of 987P fimbriae of Escherichia coli.
            #accession A49891
            #status preliminary
            #molecule_type DNA
            #residues 1-835 #label SCH
            #cross-references GB:L22659
GENETICS   fasD
            #gene transmembrane protein
            #length 835 #molecular-weight 92354 #checksum 6404
SUMMARY

```

Query Match 61.7%; Score 50; DB 7; Length 835;
Best Local Similarity 50.0%; Pred. No. 2.56e+00;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 324 nkeadgsehshf 335
:||||:|:
Qy 1 DVKEADPTGHSY 12

RESULT 10
ENTRY carboxypeptidase A (EC 3.4.17.1) CPA3 precursor - human
TITLE carboxypeptidase A3
ALTERNATE NAMES mast cell carboxypeptidase A3
ORGANISM Homo sapiens #common name man
DATE 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
01-Mar-1996

ACCESSIONS A43929; A39246; A45759
REFERENCE A43929
#authors Reynolds, D.S.; Gurley, D.S.; Austen, K.F.
#journal J. Clin. Invest. (1992) 89:273-282
#title Cloning and characterization of the novel gene for mast cell
carboxypeptidase A.
#cross-references MUID:92105393
#accession A43929
#molecule_type DNA
#residues 1-417 #label REY
#cross-references GB:M73716
#experimental_source mast cell
#note the authors translated the codon CGC for residue 231 as
Thr

REFERENCE A39246
#authors Reynolds, D.S.; Gurley, D.S.; Stevens, R.L.; Sugarbaker,
D.J.; Austen, K.F.; Serafin, W.E.
#journal Proc. Natl. Acad. Sci. U.S.A. (1989) 86:9480-9484
#title Cloning of cDNAs that encode human mast cell carboxypeptidase
A, and comparison of the protein with mouse mast cell
carboxypeptidase A and rat pancreatic carboxypeptidases.
#cross-references MUID:90083291
#accession A39246
#molecule_type mRNA
#residues 1-417 #label RE2
#cross-references GB:M27717

REFERENCE A45759
#authors Goldstein, S.M.; Kaempfer, C.E.; Kealey, J.T.; Wintroub, B.O.
#journal J. Clin. Invest. (1989) 83:1630-1636
#title Human mast cell carboxypeptidase. Purification and
characterization.
#accession A45759
#molecule_type protein
#residues 110-137 #label GOL

GENETICS GDB:CPA3
#gene GDB:CPA3
#cross-references GDB:G00-125-231
#map_position 3q21.3-q25
#introns 23/2; 48/3; 90/2; 124/3; 158/3; 192/3; 229/3; 260/1; 327/3;
356/1

CLASSIFICATION #superfamily carboxypeptidase
KEYWORDS hydrolase; metallo-carboxypeptidase; metalloprotein; protein
digestion; zinc

FEATURE
1-15 #domain signal sequence #status predicted #label SIG\
16-109 #domain activation peptide #status predicted #label ACT\
110-417 #product carboxypeptidase A, mast cell #status predicted
#label MAT\
176,179,304 #binding site zinc (His, Glu, His) #status predicted\
245-268 #disulfide_bonds #status predicted
SUMMARY #length 417 #molecular-weight 48700 #checksum 5283

Query Match 60.5%; Score 49; DB 4; Length 417;
Best Local Similarity 66.7%; Pred. No. 4.13e+00;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 105 dvkedipgrhshy 116
|||||
Qy 1 DVKEADPTGHSY 12

RESULT 11
ENTRY genome polyprotein - bovine viral diarrhoea virus (strain
SD-1)
TITLE #formal_name bovine viral diarrhoea virus, BVDV
ORGANISM 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change
08-Dec-1994
DATE A44217
ACCESSIONS A44217
REFERENCE A44217
#authors Deng, R.; Brock, K.V.
#journal Virology (1992) 191:867-879
#title Molecular cloning and nucleotide sequence of a pestivirus
genome, noncytopathic bovine viral diarrhoea virus strain
SD-1.

#accession A44217
#molecule_type genomic RNA
#residues 1-3898 #label DEN
#cross-references GB:M96751
#note this polyprotein may be cleaved into several mature
proteins, including p20 protein, p14 protein, gp48
protein, gp25 protein, gp53 protein, p54 protein, p80
protein, p10 protein, p38 protein, and p75 protein;
the cleavage sites are not reported

CLASSIFICATION #superfamily pestivirus genome polyprotein
KEYWORDS glycoprotein; polyprotein; RNA binding; zinc finger
FEATURE
253-265 #region hydrophobic\
347-362 #region hydrophobic\
556-670 #region hydrophobic\
675-694 #region hydrophobic\
1031-1046 #region hydrophobic\
1074-1099 #region hydrophobic\
1149-1164 #region hydrophobic\
1217-1238 #region hydrophobic\
1252-1269 #region hydrophobic\
1271-1292 #region hydrophobic\
1293-1304 #region hydrophobic\
1357-1373 #region hydrophobic\
1484-1512 #region zinc finger motif\
2562-2582 #region hydrophobic\
365,370,413,487,

597,809,878,922,
990,1357,1419,1713,
2134,2217,2494,
2682,2751,2891,
2988,3688,3777,
3793

#binding site carbohydrate (Asn) (covalent) #status
predicted

SUMMARY #length 3898 #molecular-weight 437805 #checksum 8806

Query Match 60.5%; Score 49; DB 3; Length 3898;
Best Local Similarity 58.3%; Pred. No. 4.13e+00;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 1132 dvkdpdgqgy 1143
||| ||| |||
Qy 1 DVKEADPTGHSY 12

RESULT 12
ENTRY S55370 #type complete
TITLE RNA polymerase II chain hRPB17 - human
ORGANISM #formal name Homo sapiens #common name man
DATE 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change
01-Sep-1995

ACCESSIONS S55370
REFERENCE S55370
#authors Shpakovski, G.; Vigneron, M.
#submission submitted to the EMBL Data Library, May 1995
#description The human polypeptides hRPB7.0, hRPB7.6 and hRPB17 are
functionally interchangeable with the RNA polymerase
subunits ABC10a, ABC10b and ABC14.5 of Saccaromyces
cerevisiae.

#accession S55370
#status preliminary
#molecule_type mRNA
#residues 1-150 #label SHP
#cross-references EMBL:249199
SUMMARY #length 150 #molecular-weight 17143 #checksum 1242

Query Match 59.3%; Score 48; DB 11; Length 150;
Best Local Similarity 50.0%; Pred. No. 6.60e+00;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Db 11 dvkdidpegkxf 22
|||: ||| |
Qy 1 DVKEADPTGHSY 12

RESULT 13
ENTRY A49334 #type complete
TITLE Ras homolog Rad - human
ORGANISM #formal name Homo sapiens #common name man
DATE 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change
07-Oct-1994

ACCESSIONS A49334
REFERENCE A49334
#authors Reynet, C.; Kahn, C.R.
#journal Science (1993) 262:1441-1444
#title Rad: a member of the Ras family overexpressed in muscle of

#accession A49334 type II diabetic humans.

#status preliminary
#molecule_type mRNA
#residues 1-269 #label REY
#cross-references GB:L24564

KEYWORDS alternative initiators

SUMMARY #length 269 #molecular-weight 29262 #checksum 9237

Query Match 59.3%; Score 48; DB 11; Length 269;
Best Local Similarity 55.6%; Pred. No. 6.60e+00;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 80 eaesaaghty 88
|||: ||| |
Qy 4 EADPTGHSY 12

RESULT 14
ENTRY A39216 #type complete
TITLE nucleotide pyrophosphatase - human
ALTERNATE_NAMES plasma cell membrane glycoprotein PC-1
ORGANISM #formal name Homo sapiens #common name man
DATE 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change
09-Mar-1996

ACCESSIONS A39216; S21706; S23587
REFERENCE A39216
#authors Buckley, M.F.; Loveland, K.A.; McKinstry, W.J.; Garson, O.M.;
Goding, J.W.
#journal J. Biol. Chem. (1990) 265:17506-17511
#title Plasma cell membrane glycoprotein PC-1. cDNA cloning of the
human molecule, amino acid sequence, and chromosomal
location.

#cross-references MUID:91009202
#accession A39216
#status preliminary
#molecule_type mRNA
#residues 1-925 #label BUC
#cross-references GB:J05654

REFERENCE S21706
#authors Funakoshi, I.; Kato, H.; Horie, K.; Yano, T.; Hori, Y.;
Kobayashi, H.; Inoue, T.; Suzuki, H.; Fukui, S.; Takahara,
M.; Kajii, T.; Yamashina, I.
#journal Arch. Biochem. Biophys. (1992) 295:180-187
#title Molecular cloning of cDNAs for human fibroblast nucleotide
pyrophosphatase.

#cross-references MUID:92246539
#accession S21706
#status not compared with conceptual translation
#molecule_type mRNA
#residues 1-925 #label FUN1
#molecule_type protein
#accession S23587
#residues 116-121;247-271,'X',273-275;279-280,'X',282-283;303-316;
362-364;449-465;482-525;529-534,'X',536-551,'X',553,
'X',555-556;597-606,'X',727-730;775-782;840-846,'XX',
849-852,'X',854-859 #label FUN2

#note it is uncertain whether Met-1 or Met-53 is the initiator
GENETICS
#map_position 6q22-q23

CLASSIFICATION #superfamily somatomedin B homology
 KEYWORDS glycoprotein; transmembrane protein
 FEATURE 77-97
 104-144 #domain transmembrane #status predicted #label TMH
 145-188 #domain somatomedin B homology #label SBH1
 179,285,341,477, #domain somatomedin B homology #label SBH2
 578,585,643,700, #binding_site carbohydrate (Asn) (covalent) #status
 731,748 predicted
 SUMMARY #length 925 #molecular-weight 104924 #checksum 7446
 Query Match 59.3%; Score 48; DB 1; Length 925;
 Best Local Similarity 66.7%; Pred. No. 6.60e+00;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 374 epdssghsy 382
 I:::IIII
 Qy 4 EADPTGHSY 12

RESULT 15
 ENTRY KIPGGU #type complete
 TITLE guanylate kinase (EC 2.7.4.8) - pig
 ORGANISM #formal name Sus scrofa domestica #common name domestic pig
 DATE 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change
 10-Nov-1995
 ACCESSIONS S23776
 REFERENCE S23776
 #authors Zschocke, P.D.; Schiltz, E.; Schulz, G.E.
 #submission submitted to the Protein Sequence Database, September 1992
 #accession S23776
 #molecule_type protein
 #residues 1-197 #label ZSC
 CLASSIFICATION #superfamily guanylate kinase; guanylate kinase homology
 KEYWORDS acetylated amino end; ATP; magnesium; monomer;
 phosphotransferase

FEATURE
 3-188 #domain guanylate kinase homology #label GK1
 10-17 #region nucleotide-binding motif A (P-loop)
 35-82 #region GMP binding #status predicted
 1 #modified_site acetylated amino end (Gly) #status
 experimental
 16 #binding site ATP (Lys) #status predicted
 SUMMARY #length 197 #molecular-weight 21789 #checksum 2414
 Query Match 58.0%; Score 47; DB 1; Length 197;
 Best Local Similarity 54.5%; Pred. No. 1.05e+01;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 187 eikkaqatgths 197
 :::I::IIII
 Qy 1 DVKEADPTGHS 11

Search completed: Thu Apr 3 11:59:40 1997
 Job time : 7 secs.

WVPSGLH (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MParch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Thu Apr 3 11:59:10 1997; MasPar time 1.75 Seconds
 127.208 Million cell updates/sec
 Tabular output not generated.

Title: >US-08-190-411A-4
 Description: (1-12) from 5541104.pep
 Perfect Score: 81
 Sequence: 1 DVKEADPTGHSY 12
 Scoring table: PAM 150
 Gap 15

Searched: 52205 seqs, 18531385 residues
 Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: swiss-prot33
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
 8:part8 9:part9 10:part10

Statistics: Mean 23.371; Variance 23.554; scale 0.992

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	81	100.0	309	5	MAG1_HUMAN	MELANOMA-ASSOCIATED A	8.25e-10
2	74	91.4	234	5	MAG8_HUMAN	MELANOMA-ASSOCIATED A	1.19e-07
3	74	91.4	315	5	MAG9_HUMAN	MELANOMA-ASSOCIATED A	1.19e-07
4	72	88.9	369	5	MAGX_HUMAN	MELANOMA-ASSOCIATED A	4.79e-07
5	71	87.7	319	5	MAGY_HUMAN	MELANOMA-ASSOCIATED A	9.52e-07
6	62	76.5	317	5	MAG4_HUMAN	MELANOMA-ASSOCIATED A	3.79e-04
7	57	70.4	347	5	MAGP_HUMAN	MELANOMA-ASSOCIATED A	8.78e-03
8	53	65.4	314	5	MAG6_HUMAN	MELANOMA-ASSOCIATED A	9.68e-02
9	52	64.2	417	3	F16P_ARATH	FRUCTOSE-1,6-BISPHOSP	1.73e-01
10	50	61.7	314	5	MAG3_HUMAN	MELANOMA-ASSOCIATED A	5.43e-01
11	50	61.7	381	3	F16P_PEA	FRUCTOSE-1,6-BISPHOSP	5.43e-01
12	50	61.7	835	3	FASD_ECOLI	OUTER MEMBRANE USHER	5.43e-01

13 49 60.5 411 3 F16P BRANA FRUCTOSE-1,6-BISPHOSP 9.49e-01
 14 49 60.5 417 2 CBPC HUMAN MAST CELL CARBOXYPEPT 9.49e-01
 15 49 60.5 3898 7 POLG_EVDVS GENOME POLYPROTEIN. 9.49e-01
 16 48 59.3 873 6 PC1_HUMAN PLASMA-CELL MEMBRANE 1.65e+00
 17 47 58.0 197 5 KGOA_PIG GUANYLATE KINASE (EC 2.83e+00
 18 47 58.0 443 4 GINA_BACCE GLUTAMINE SYNTHETASE 2.83e+00
 19 47 58.0 443 4 GINA_BACSU GLUTAMINE SYNTHETASE 2.83e+00
 20 47 58.0 445 4 GINA_LACDE GLUTAMINE SYNTHETASE 2.83e+00
 21 47 58.0 497 6 PEN3_ADE12 PENTON PROTEIN (VIRIO 2.83e+00
 22 47 58.0 633 9 XRCX_HUMAN DNA-REPAIR PROTEIN XR 2.83e+00
 23 46 56.8 147 6 PA24_BUNMO PHOSPHOLIPASE A2, BET 4.82e+00
 24 46 56.8 583 1 ARSA_ECOLI ARSENICAL PUMP-DRIVEN 4.82e+00
 25 45 55.6 581 6 PBP2_NEIME PENICILLIN-BINDING PR 8.13e+00
 26 45 55.6 581 6 PBP2_NEIGO PENICILLIN-BINDING PR 8.13e+00
 27 45 55.6 725 6 MYT1_HUMAN MYELIN TRANSCRIPTION 8.13e+00
 28 45 55.6 1033 8 TIRI_ECOLI TYPE I RESTRICTION EN 8.13e+00
 29 44 54.3 22 10 YHVA_LACHE HYPOTHETICAL PROTEIN 1.36e+01
 30 44 54.3 222 10 YHVA_LACHE HYPOTHETICAL 23.7 KD 1.36e+01
 31 44 54.3 261 1 1431_VICFA 14-3-3-LIKE PROTEIN V 1.36e+01
 32 44 54.3 469 4 GINI_RHLIV GLUTAMINE SYNTHETASE 1.36e+01
 33 44 54.3 488 8 SUOX_RAT SULFITE OXIDASE PRECU 1.36e+01
 34 44 54.3 539 2 COMM_SYN7 CARBON DIOXIDE CONCEN 1.36e+01
 35 44 54.3 789 1 ACOX_YEAST PUTATIVE ACONITASE IN 1.36e+01
 36 44 54.3 826 9 VILI_HUMAN VILLIN. 1.36e+01
 37 44 54.3 1173 9 TSP1_XENLA THROMBOSPONDIN 1 PREC 1.36e+01
 38 43 53.1 176 8 RL5_HAIMA 50S RIBOSOMAL PROTEIN 2.24e+01
 39 43 53.1 228 7 RL1_THETH 50S RIBOSOMAL PROTEIN 2.24e+01
 40 43 53.1 326 10 YKX2_CAEEL HYPOTHETICAL 34.6 KD 2.24e+01
 41 43 53.1 362 10 YCHF_HAEIN PROBABLE GTP-BINDING 2.24e+01
 42 43 53.1 559 7 PPBI_MOUSE ALKALINE PHOSPHATASE, 2.24e+01
 43 43 53.1 690 2 CGCC_BOVIN CGMP-GATED CATION CHA 2.24e+01
 44 43 53.1 878 10 YB9X_YEAST HYPOTHETICAL TRP-ASP 2.24e+01
 45 43 53.1 3396 7 POLG_DENIS GENOME POLYPROTEIN (C 2.24e+01

ALIGNMENTS

RESULT 1
 ID MAG1 HUMAN STANDARD; PRT; 309 AA.
 AC P43355;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE MELANOMA-ASSOCIATED ANTIGEN 1 (MAGE-1 ANTIGEN) (ANTIGEN MZ2-E).
 GN MAGE1.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 92086861.
 RA VAN DER BRUGEN P., TRAVERSARI C., CHOMEZ P., LURQUIN C., DE PLAEN E.,
 RA VAN DEN EYNDE B., KNUTH A., BOON T.;
 RL SCIENCE 254:1643-1647(1991).
 [2]
 RN SEQUENCE FROM N.A.
 RP TISSUE=SKIN;
 RX MEDLINE; 94311935.
 RA DING M., BECK R.J., KELLER C.J., FENTON R.G.;
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 202:549-555(1994).

RN [3]
 RP MUTAGENESIS.
 RC TISSUE=BLOOD;
 RX MEDLINE; 94157413.
 RA GAUGLER B., VAN DEN EYNDE B., VAN DER BRUGEN P., ROMERO P.,
 RA GAFORIO J.-J., DE PLAEN E., LETHE B., BRASSEUR F., BOON T.;
 RL J. EXP. MED. 179:921-930(1994).
 CC -!- FUNCTION: NOT KNOWN, THOUGH MAY PLAY A ROLE IN EMBRYONAL
 CC DEVELOPMENT AND TUMOR TRANSFORMATION OR ASPECTS OF TUMOR
 CC PROGRESSION. ANTIGEN RECOGNIZED ON A MELANOMA BY AUTOLOGOUS
 CC CYTOLYTIC T LYMPHOCYTES.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES,
 CC SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LUNG
 CC CARCINOMA AND BREAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT
 CC FOR TESTES. NEVER EXPRESSED IN KIDNEY TUMORS, LEUKEMIAS AND
 CC LYMPHOMAS.
 CC -!- POLYMORPHISM: THE VARIANT AT POSITION 32 LIKELY REPRESENTS A
 CC POLYMORPHISM OF THE MAGE-1 GENE.
 CC -!- SIMILARITY: BELONGS TO THE MAGE FAMILY.
 DR EMBL; M77481; G416115; -.
 KW MIM; 600186; 11TH EDITION.
 FT VARIANT 32 32
 FT DOMAIN 33 36 POLY-SER.
 FT MUTAGEN 163 163 D->A: ABOLISHES HLA-A1 BINDING.
 FT MUTAGEN 169 169 Y->A: ABOLISHES HLA-A1 BINDING.
 SQ SEQUENCE 309 AA; 34342 MW; E6CB1300 CRC32;

Query Match 100.0%; Score 81; DB 5; Length 309;
 Best Local Similarity 100.0%; Pred. No. 8.25e-10;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 158 dvkeadptghsy 169
 |||||
 Qy 1 DVKEADPTGHSY 12

RESULT 2
 ID MAG8 HUMAN STANDARD; PRT; 234 AA.
 AC P43361;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE MELANOMA-ASSOCIATED ANTIGEN 8 (MAGE-8 ANTIGEN).
 GN MAGE8.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 95012457.
 RA DE PLAEN E., ARDEN K., TRAVERSARI C., GAFORIO J.-J., SZIKORA J.-P.,
 RA DE SMET C., BRASSEUR F., VAN DER BRUGEN P., LETHE B., LURQUIN C.,
 RA BRASSEUR R., CHOMEZ P., DE BACKER O., CAUVENEE W., BOON T.;
 RL IMMUNOGNETICS 40:360-369(1994).
 CC -!- FUNCTION: NOT KNOWN, THOUGH MAY PLAY A ROLE IN EMBRYONAL
 CC DEVELOPMENT AND TUMOR TRANSFORMATION OR ASPECTS OF TUMOR
 CC PROGRESSION.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES,
 CC SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LUNG

CC CARCINOMA AND BREAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT
CC FOR TESTES AND PLACENTA.

CC -!- SIMILARITY: BELONGS TO THE MAGE FAMILY.

DR EMBL; U10693; G533526; --
RW ANTIGEN; MULTIGENE FAMILY; TUMOR ANTIGEN.

FT DOMAIN 40 43 POLY-SER.

SQ SEQUENCE 234 AA; 25197 MW; D4931BC3 CRC32;

Query Match 91.4%; Score 74; DB 5; Length 234;

Best Local Similarity 83.3%; Pred. No. 1.19e-07; Indels 0; Gaps 0;
Matches 10; Conservative 1; Mismatches 1;

Db 168 dvkevdpaghsy 179

QY 1 DVKEADPTGHSY 12
||||| 11:|||||

RESULT 3

ID MAG9_HUMAN STANDARD; PRT; 315 AA.

AC P43362;

DT 01-NOV-1995 (REL. 32, CREATED)

DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)

DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)

DE MELANOMA-ASSOCIATED ANTIGEN 9 (MAGE-9 ANTIGEN).

GN MAGE9

OS HOMO SAPIENS (HUMAN).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; PRIMATES.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 95012457.

RA DE PLAEN E., ARDEN K., TRAVERSARI C., GAFORIO J.J., SZIKORA J.-P.,

RA DE SMET C., BRASSEUR F., VAN DER BRUGGEN P., LETHE B., LURQUIN C.,

RA BRASSEUR R., CHOMEZ P., DE BACKER O., CAVEENE W., BOON T.;

RL IMMUNOGENETICS 40:360-369(1994).

CC -!- FUNCTION: NOT KNOWN, THOUGH MAY PLAY A ROLE IN EMBRYONAL

CC DEVELOPMENT AND TUMOR TRANSFORMATION OR ASPECTS OF TUMOR

CC PROGRESSION.

CC -!- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES,
CC SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LUNG
CC CARCINOMA AND BREAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT

CC FOR TESTES AND PLACENTA.

CC -!- SIMILARITY: BELONGS TO THE MAGE FAMILY.

DR EMBL; U10694; G533528; --

KW ANTIGEN; MULTIGENE FAMILY; TUMOR ANTIGEN.

FT DOMAIN 34 37 POLY-GLU.

FT DOMAIN 87 90 POLY-GLU.

SQ SEQUENCE 315 AA; 35088 MW; 7DC3228E CRC32;

Query Match 91.4%; Score 74; DB 5; Length 315;

Best Local Similarity 83.3%; Pred. No. 1.19e-07;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 164 dvkevdpaghsy 175

QY 1 DVKEADPTGHSY 12
||||| 11:|||||

RESULT 4

ID MAG9_HUMAN STANDARD; PRT; 369 AA.

AC P43363;

DT 01-NOV-1995 (REL. 32, CREATED)

DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)

DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)

DE MELANOMA-ASSOCIATED ANTIGEN 10 (MAGE-10 ANTIGEN).

GN MAGE10.

OS HOMO SAPIENS (HUMAN).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; PRIMATES.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 95012457.

RA DE PLAEN E., ARDEN K., TRAVERSARI C., GAFORIO J.J., SZIKORA J.-P.,

RA DE SMET C., BRASSEUR F., VAN DER BRUGGEN P., LETHE B., LURQUIN C.,

RA BRASSEUR R., CHOMEZ P., DE BACKER O., CAVEENE W., BOON T.;

RL IMMUNOGENETICS 40:360-369(1994).

CC -!- FUNCTION: NOT KNOWN, THOUGH MAY PLAY A ROLE IN EMBRYONAL

CC DEVELOPMENT AND TUMOR TRANSFORMATION OR ASPECTS OF TUMOR

CC PROGRESSION.

CC -!- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES,
CC SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LUNG
CC CARCINOMA AND BREAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT

CC FOR TESTES AND PLACENTA.

DR EMBL; U10685; G533511; --

KW ANTIGEN; MULTIGENE FAMILY; TUMOR ANTIGEN.

FT DOMAIN 54 62 POLY-SER.

SQ SEQUENCE 369 AA; 40766 MW; D11E1870 CRC32;

Query Match 88.9%; Score 72; DB 5; Length 369;

Best Local Similarity 83.3%; Pred. No. 4.79e-07;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 190 dvkevdpaghsf 201

QY 1 DVKEADPTGHSY 12
||||| 11:|||||

RESULT 5

ID MAGY_HUMAN STANDARD; PRT; 319 AA.

AC P43364;

DT 01-NOV-1995 (REL. 32, CREATED)

DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)

DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)

DE MELANOMA-ASSOCIATED ANTIGEN 11 (MAGE-11 ANTIGEN).

GN MAGE11.

OS HOMO SAPIENS (HUMAN).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; PRIMATES.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 95012457.

RA DE PLAEN E., ARDEN K., TRAVERSARI C., GAFORIO J.J., SZIKORA J.-P.,

RA DE SMET C., BRASSEUR F., VAN DER BRUGGEN P., LETHE B., LURQUIN C.,

RA BRASSEUR R., CHOMEZ P., DE BACKER O., CAVEENE W., BOON T.;

RL IMMUNOGENETICS 40:360-369(1994).

CC -!- FUNCTION: NOT KNOWN, THOUGH MAY PLAY A ROLE IN EMBRYONAL

CC DEVELOPMENT AND TUMOR TRANSFORMATION OR ASPECTS OF TUMOR

CC PROGRESSION.

CC -!- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES,
CC SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LUNG

CC CARCINOMA AND BREAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT
CC FOR TESTES AND PLACENTA.

CC -!- SIMILARITY: BELONGS TO THE MAGE FAMILY.

DR EMBL; U10686; G533513; --

RW ANTIGEN; MULTIGENE FAMILY; TUMOR ANTIGEN.

SQ SEQUENCE 319 AA; 35536 MW; E3DBDEF CRC32;

Query Match 87.7%; Score 71; DB 5; Length 319;

Best Local Similarity 83.3%; Pred. No. 9.52e-07;

Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 168 dvkevdptshy 179

||||| |||:||||

QY 1 DVKEADPTGHSY 12

RESULT 6
ID MAG4 HUMAN STANDARD; PRT; 317 AA.

AC P43358; (REL. 32, CREATED)

DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)

DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)

DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)

DE MELANOMA-ASSOCIATED ANTIGEN 4 (MAGE-4 ANTIGEN) (MAGE-X2).

GN MAGE4.

OS HOMO SAPIENS (HUMAN).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; PRIMATES.

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=BLOOD;

RX MEDLINE; 95012457.

RA DE PLAEN E., ARDEN K., TRAVERSARI C., GAFORIO J.J., SZIKORA J.-P.,

RA DE SNET C., BRASSEUR F., VAN DER BRUGGEN P., LETHE B., LURQUIN C.,

RA BRASSEUR R., CHOMEZ P., DE BACKER O., CAVENEY W., BOON T.;

RL IMMUNOGENETICS 40:360-369(1994).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=SKIN;

RX MEDLINE; 94311935.

RA DING M., BECK R.J., KELLER C.J., FENTON R.G.;

RA BIOCHEMA. BIOPHYS. RES. COMMUN. 202:549-555(1994).

CC -!- FUNCTION: NOT KNOWN. THOUGH MAY PLAY A ROLE IN EMBRYONAL

CC DEVELOPMENT AND TUMOR TRANSFORMATION OR ASPECTS OF TUMOR

CC PROGRESSION.

CC -!- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES,

CC SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LONG

CC CARCINOMA AND BREAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT

CC FOR TESTES AND PLACENTA.

CC -!- SIMILARITY: BELONGS TO THE MAGE FAMILY. STRONG SIMILARITY WITH

CC MAGE-1.

DR EMBL; U10687; G533515; --

DR EMBL; U10688; G533517; --

DR EMBL; U10340; G49124; --

KW ANTIGEN; MULTIGENE FAMILY; POLYMORPHISM; TUMOR ANTIGEN.

FT DOMAIN 41 44 POLY-SER.

FT VARIANT 173 173 T -> A.

FT CONFLICT 307 307 E -> Q (IN REF. 2).

SQ SEQUENCE 317 AA; 34929 MW; 3CE38AF9 CRC32;

Query Match 76.5%; Score 62; DB 5; Length 317;

Best Local Similarity 66.7%; Pred. No. 3.79e-04;

Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 166 dvkevdptshy 177

||||| |||:||||

QY 1 DVKEADPTGHSY 12

RESULT 7

ID MAGP HUMAN STANDARD; PRT; 347 AA.

AC P43366; (REL. 32, CREATED)

DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)

DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)

DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)

DE MELANOMA-ASSOCIATED ANTIGEN XP (MAGE-XP ANTIGEN).

GN MAGELI OR MAGEXP.

OS HOMO SAPIENS (HUMAN).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; PRIMATES.

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=TESTES;

RA MUSCATELLI F., WALKER A.P., DE PLAEN E., STAFFORD A.N., MONACO A.P.;

RL PROC. NATL. ACAD. SCI. U.S.A. 92:4987-4991(1995).

CC -!- TISSUE SPECIFICITY: EXPRESSED ONLY IN TESTIS.

CC -!- SIMILARITY: BELONGS TO THE MAGE FAMILY.

DR EMBL; X82539; G608993; --

DR MIM; 600619; 11TH EDITION.

KW ANTIGEN; MULTIGENE FAMILY.

SQ SEQUENCE 347 AA; 39152 MW; A041BAB2 CRC32;

Query Match 70.4%; Score 57; DB 5; Length 347;

Best Local Similarity 50.0%; Pred. No. 8.78e-03;

Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 164 dlkednpsshty 175

||||| |||:||||

QY 1 DVKEADPTGHSY 12

RESULT 8

ID MAG6 HUMAN STANDARD; PRT; 314 AA.

AC P43360; (REL. 32, CREATED)

DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)

DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)

DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)

DE MELANOMA-ASSOCIATED ANTIGEN 6 (MAGE-6 ANTIGEN) (MAGE3B).

GN MAGE6.

OS HOMO SAPIENS (HUMAN).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; PRIMATES.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 95012457.

RA DE PLAEN E., ARDEN K., TRAVERSARI C., GAFORIO J.J., SZIKORA J.-P.,

RA DE SNET C., BRASSEUR F., VAN DER BRUGGEN P., LETHE B., LURQUIN C.,

RA BRASSEUR R., CHOMEZ P., DE BACKER O., CAVENEY W., BOON T.;

RL IMMUNOGENETICS 40:360-369(1994).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=SKIN;
RX MEDLINE; 94311935.
RA DING M., BECK R.J., KELLER C.J., FENTON R.G.;
RL BIOCHEM. BIOPHYS. RES. COMMUN. 202:549-555(1994).
CC -!- FUNCTION: NOT KNOWN, THOUGH MAY PLAY A ROLE IN TUMOR
CC OR ASPECTS OF TUMOR PROGRESSION.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES,
CC SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LUNG
CC CARCINOMA AND BREAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT
CC FOR TESTES.
CC -!- SIMILARITY: BELONGS TO THE MAGE FAMILY. STRONG SIMILARITY TO
CC MAGE-3.
DR EMBL; U10691; G533523; -.
DR EMBL; U10339; G499122; -.
KW ANTIGEN; MULTIGENE FAMILY; TUMOR ANTIGEN.
FT DOMAIN 40 43 POLY-SER.
SQ SEQUENCE 314 AA; 34891 MW; B7125E97 CRC32;

Query Match 65.4%; Score 53; DB 5; Length 314;
Best Local Similarity 50.0%; Pred. No. 9.68e-02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Db 165 elmevdpigvwy 176
QY 1 DVKEADPTGHSY 12

RESULT 9
ID F16P ARATH STANDARD; PRT; 417 AA.
AC P25831;
DT 01-MAY-1992 (REL. 22, CREATED)
DT 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (EC 3.1.3.11)
DE (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE).
GN FBP.
OS ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
OC EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
OC CAPPARALES; CRUCIFERAE.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91329733.
RA HORSNELL P.R., RAINES C.A.;
RL PLANT MOL. BIOL. 17:185-186(1991).
CC -!- CATALYTIC ACTIVITY: D-FRUCTOSE 1,6-BISPHOSPHATE + H(2)O =
CC D-FRUCTOSE 6-PHOSPHATE + ORTHOPHOSPHATE.
CC -!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -!- PATHWAY: THE CHLOROPLAST ISOZYME TAKES PART IN THE REGENERATION OF
CC RIBULOSE BISPHOSPHATE IN THE PHOTOSYNTHETIC CARBON REDUCTION
CC CYCLE (CALVIN CYCLE).
CC -!- INDUCTION: LIGHT ACTIVATION THROUGH PH CHANGES, MG(2+) LEVELS
CC AND ALSO BY LIGHT-MODULATED REDUCTION OF ESSENTIAL DISULPHIDE
CC GROUPS VIA THE FERREDOXIN-THIOREDOXIN F SYSTEM (BY SIMILARITY).
CC -!- IN PLANTS THERE ARE TWO FBPAE ISOZYMES: ONE IN THE CYTOSOL AND
CC THE OTHER IN THE CHLOROPLAST.
DR EMBL; X58148; G11242; -.
DR PIR; S16582; S16582.
DR HSSP; P00636; IFBH.
DR PROSITE; PS00124; FBPAE.

KW HYDROLASE; CARBOHYDRATE METABOLISM; MULTIGENE FAMILY; CHLOROPLAST;
KW TRANSIT PEPTIDE; CALVIN CYCLE.
FT TRANSIT 1 59 CHLOROPLAST (POTENTIAL).
FT CHAIN 60 417 FRUCTOSE-1,6-BISPHOSPHATASE.
FT ACT_SITE 359 359 BY SIMILARITY.
FT DISULFID 233 238 REDOX-ACTIVE (LIGHT-MODULATED) (BY
FT SIMILARITY).
SQ SEQUENCE 417 AA; 45178 MW; 9A30B20C CRC32;

Query Match 64.2%; Score 52; DB 3; Length 417;
Best Local Similarity 50.0%; Pred. No. 1.73e-01;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
Db 314 dlkdpgptgkpy 325
QY 1 DVKEADPTGHSY 12

RESULT 10
ID MAG3 HUMAN STANDARD; PRT; 314 AA.
AC P43357;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE MELANOMA-ASSOCIATED ANTIGEN 3 (MAGE-3 ANTIGEN) (ANTIGEN MZ2-D).
GN MAGE3.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS.
RC TISSUE=BLOOD;
RX MEDLINE; 94157413.
RA GAUGLER B., VAN DEN EYNDE B., VAN DER BRUGGEN P., ROMERO P.,
RA GAFORIO J.J., DE PLAEN E., LETHE B., BRASSEUR F., BOON T.;
RL J. EXP. MED. 179:921-930(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=SKIN;
RX MEDLINE; 94311935.
RA DING M., BECK R.J., KELLER C.J., FENTON R.G.;
RL BIOCHEM. BIOPHYS. RES. COMMUN. 202:549-555(1994).
CC -!- FUNCTION: NOT KNOWN, THOUGH MAY PLAY A ROLE IN EMBRYONAL
CC DEVELOPMENT AND TUMOR TRANSFORMATION OR ASPECTS OF TUMOR
CC PROGRESSION. ANTIGEN RECOGNIZED ON A MELANOMA BY AUTOLOGOUS
CC CYTOLYTIC T LYMPHOCYTES.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES,
CC SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LUNG
CC CARCINOMA AND BREAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT
CC FOR TESTES AND PLACENTA. NEVER EXPRESSED IN KIDNEY TUMORS,
CC LEUKEMIAS AND LYMPHOMAS.
CC -!- SIMILARITY: BELONGS TO THE MAGE FAMILY.
CC EMBL; U03735; G468826; -.
DR ANTIGEN; MULTIGENE FAMILY; TUMOR ANTIGEN.
KW DOMAIN 40 43 POLY-SER.
FT MUTAGEN 170 170 D->A: ABOLISHES HLA-A1 BINDING.
FT MUTAGEN 176 176 Y->A: ABOLISHES HLA-A1 BINDING.
SQ SEQUENCE 314 AA; 34747 MW; AC557A64 CRC32;

Query Match 61.7%; Score 50; DB 5; Length 314;

Best Local Similarity 50.0%; Pred. No. 5.43e-01;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 165 elmevdpighly 176
:::| || || |
Qy 1 DVKEADPTGHSY 12

RESULT 11
ID F16P PEA STANDARD; PRT; 381 AA.
AC P46275;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (EC 3.1.3.11)
DE (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) (FRAGMENT).
GN FBP.
OS PISUM SATIVUM (GARDEN PEA).
OC EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE; FABALES;
OC FABACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. LINCOLN; TISSUE=LEAF;
RX MERRILL; 94297517.
RA CARRASCO J.L., CHUECA A., PRADO F.E., HERMOSO R., LAZARO J.J.,
RA RAMOS J.L., SAREAWY M., LOPEZ GORGE J.;
RL PLANTA 193:494-501 (1994).
CC -!- CATALYTIC ACTIVITY: D-FRUCTOSE 1,6-BISPHOSPHATE + H(2)O =
CC D-FRUCTOSE 6-PHOSPHATE + ORTHOPHOSPHATE.
CC -!- SUBUNIT: HOMOTETRAMER.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST STROMA.
CC -!- PATHWAY: THE CHLOROPLAST ISOZYME TAKES PART IN THE REGENERATION OF
CC RIBULOSE BISPHOSPHATE IN THE PHOTOSYNTHETIC CARBON REDUCTION
CC CYCLE (CALVIN CYCLE).
CC -!- INDUCTION: LIGHT ACTIVATION THROUGH PH CHANGES, MG(2+) LEVELS
CC AND ALSO BY LIGHT-MODULATED REDUCTION OF ESSENTIAL DISULFIDE
CC GROUPS VIA THE FERREDOXIN-THIOREDOXIN F SYSTEM (BY SIMILARITY).
CC -!- IN PLANTS THERE ARE TWO FBPAE ISOZYMES: ONE IN THE CYTOSOL AND
CC THE OTHER IN THE CHLOROPLAST.
DR EMBL; X68826; G20717; -.
KW HYDROLASE; CARBOHYDRATE METABOLISM; MULTIGENE FAMILY; CHLOROPLAST;
KW TRANSIT PEPTIDE; CALVIN CYCLE.
FT NON TER 1 1
FT TRANSIT <1 24 CHLOROPLAST (POTENTIAL).
FT CHAIN 25 381 FRUCTOSE-1,6-BISPHOSPHATASE.
FT ACT SITE 323 323 BY SIMILARITY.
FT DISULFID 197 202 REDOX-ACTIVE (LIGHT-MODULATED) (BY
FT SIMILARITY).
SQ SEQUENCE 381 AA; 41821 MW; ABSD3B2E CRC32;

Query Match 61.7%; Score 50; DB 3; Length 381;
Best Local Similarity 50.0%; Pred. No. 5.43e-01;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 278 dlkepgpsgkpy 289
|:|:|:|:|:|
Qy 1 DVKEADPTGHSY 12

RESULT 12
ID FASD ECOLI STANDARD; PRT; 835 AA.
AC P46080;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE OUTER MEMBRANE USHER PROTEIN FASD PRECURSOR.
GN FASD.

OS ESCHERICHIA COLI.
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC ENTEROBACTERIACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=987;
RX MEDLINE; 94148769.
RA SCHIFFERLI D.M., ALBUTZ M.A.;
RL J. BACTERIOL. 176:1099-1110 (1994).
CC -!- FUNCTION: INVOLVED IN THE EXPORT AND ASSEMBLY OF THE 987P
CC FIMBRIAE SUBUNITS ACROSS THE OUTER MEMBRANE.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
CC -!- SIMILARITY: TO OTHER FIMBRIAL EXPORT USHER PROTEINS.
DR EMBL; L22659; G437336; -.
DR PROSITE; PS01151; FIMBRIAL USHER.
KW OUTER MEMBRANE; TRANSMEMBRANE; FIMBRIA; TRANSPORT; SIGNAL.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 835 OUTER MEMBRANE USHER PROTEIN FASD.
FT DISULFID 810 834 POTENTIAL.
FT SEQUENCE 835 AA; 92354 MW; D8FBD031 CRC32;

Query Match 61.7%; Score 50; DB 3; Length 835;
Best Local Similarity 50.0%; Pred. No. 5.43e-01;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 324 nikedgsehsf 335
:::|:|:|:|:|
Qy 1 DVKEADPTGHSY 12

RESULT 13
ID F16P BRANA STANDARD; PRT; 411 AA.
AC Q07204;
DT 01-OCT-1994 (REL. 30, CREATED)
DT 01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (EC 3.1.3.11)
DE (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE).
GN FBP.
OS BRASSICA NAPUS (RAPE).
OC EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
OC CAPPARALEAE; CRUCIFERAE.
RN [1]
RP SEQUENCE FROM N.A.
RA RODRIGUEZ SUAREZ R.J., WOLOSIOK R.A.;
RL SUBMITTED (MAY-1993) TO EMBL/GENBANK/DDBJ DATA BANKS.
CC -!- CATALYTIC ACTIVITY: D-FRUCTOSE 1,6-BISPHOSPHATE + H(2)O =
CC D-FRUCTOSE 6-PHOSPHATE + ORTHOPHOSPHATE.
CC -!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST STROMA.
CC -!- PATHWAY: THE CHLOROPLAST ISOZYME TAKES PART IN THE REGENERATION OF
CC RIBULOSE BISPHOSPHATE IN THE PHOTOSYNTHETIC CARBON REDUCTION

CC -!- INDUCTION: LIGHT ACTIVATION THROUGH PH CHANGES, MG(2+) LEVELS
CC AND ALSO BY LIGHT-MODULATED REDUCTION OF ESSENTIAL DISULFIDE
CC GROUPS VIA THE FERREDOXIN-THIOREDOXIN F SYSTEM (BY SIMILARITY).
CC -!- IN PLANTS THERE ARE TWO FBPAE ISOZYMES: ONE IN THE CYTOSOL AND
CC THE OTHER IN THE CHLOROPLAST.
CC EMBL; L15303; G289367; -.
DR HSP; P00636; IFRP.
DR PROSITE; PS00124; FBPAE.
KW HYDROLASE; CARBOHYDRATE METABOLISM; MULTIGENE FAMILY; CHLOROPLAST;
KW TRANSIT PEPTIDE; CALVIN CYCLE.
FT TRANSIT 1 53 CHLOROPLAST (BY SIMILARITY).
FT CHAIN 54 411 FRUCTOSE-1,6-BISPHOSPHATASE.
FT ACT SITE 353 353 BY SIMILARITY.
FT DISULFID 227 232 REDOX-ACTIVE (LIGHT-MODULATED) (BY
FT SIMILARITY).
SQ SEQUENCE 411 AA; 44446 MW; BFBD2BCD CRC32;

Query Match 60.5%; Score 49; DB 3; Length 411;
Best Local Similarity 41.7%; Pred. No. 9.49e-01;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
Db 308 dldkdpqskpy 319
Qy 1 DVKEADPTGHSY 12
I::: I:: I::

RESULT 14
ID CBPC HUMAN STANDARD; PRT; 417 AA.
AC P15088;
DT 01-APR-1990 (REL. 14, CREATED)
DT 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE MAIST CELL CARBOXYPEPTIDASE A PRECURSOR (EC 3.4.17.1) (MC-CPA)
DE (CARBOXYPEPTIDASE A3).
CN CPA3.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RC TISSUE=LUNG;
RA REYNOLDS D.S., GURLEY D.S., STEVENS R.L., SUGARBAKER D.J.,
RA AUSTEN K.F., SERAFIN W.E.;
RL J. CLIN. INVEST. 83:1630-1636(1989).
RL PROC. NATL. ACAD. SCI. U.S.A. 86:9480-9484(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=MAST CELLS;
RA MEDLINE; 92105393.
RA REYNOLDS D.S., GURLEY D.S., AUSTEN K.F.;
RL J. CLIN. INVEST. 89:273-282(1992).
RN [3]
RP SEQUENCE OF 110-137.
RX MEDLINE; 89214692.
RA GOLDSTEIN S.M., KAEMPFER C.E., KEALEY J.T., WINTROUB B.U.;
RL J. CLIN. INVEST. 83:1630-1636(1989).
CC -!- CATALYTIC ACTIVITY: PEPTIDYL-L-AMINO ACID + H(2)O = PEPTIDE +
CC L-AMINO ACID.
CC -!- SUBCELLULAR LOCATION: SECRETORY GRANULES.

CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M14; ALSO KNOWN AS THE
CC ZINC CARBOXYPEPTIDASE FAMILY.

DR EMBL; M27717; G179934; -.
DR EMBL; M73720; G187442; -.
DR EMBL; M73716; G187442; JOINED.
DR EMBL; M73717; G187442; JOINED.
DR EMBL; M73718; G187442; JOINED.
DR EMBL; M73719; G187442; JOINED.
DR PIR; A43929; A43929.
DR HSP; P09955; IPEA.
DR MIM; I14851; 11TH EDITION.
DR PROSITE; PS00132; CARBOXYPEPT ZN 1.
DR PROSITE; PS00133; CARBOXYPEPT ZN 2.
KW HYDROLASE; CARBOXYPEPTIDASE; ZINC; ZMOGEN; SIGNAL.

FT SIGNAL 1 15
FT PROPEP 16 109 ACTIVATION PEPTIDE.
FT CHAIN 110 417 MAST CELL CARBOXYPEPTIDASE A.
FT METAL 176 176 ZINC (BY SIMILARITY).
FT METAL 179 179 ZINC (BY SIMILARITY).
FT METAL 304 304 ZINC (BY SIMILARITY).
FT ACT SITE 378 378 NUCLEOPHILE (BY SIMILARITY).
FT DISULFID 173 186 BY SIMILARITY.
FT DISULFID 245 268 BY SIMILARITY.
SQ SEQUENCE 417 AA; 48700 MW; 848CEC99 CRC32;

Query Match 60.5%; Score 49; DB 2; Length 417;
Best Local Similarity 66.7%; Pred. No. 9.49e-01;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Db 105 dvkedipgrhsy 116
Qy 1 DVKEADPTGHSY 12
I::: I:: I::

RESULT 15
ID POLG BVDVS STANDARD; PRT; 3898 AA.
AC Q01439;
DT 01-JUL-1993 (REL. 26, CREATED)
DT 01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE GENOME POLYPROTEIN.
OS BOVINE VIRAL DIARRHEA VIRUS (STRAIN SD-1) (BVDV) (MUCOSAL DISEASE
OS VIRUS).
OC VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; FLAVIVIRIDAE;
OC PESTIVIRUSES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93079889.
RX DENG R., BROCK K.V.;
RL VIROLOGY 191:867-869(1992).
CC -!- FUNCTION: PESTIVIRUS P80 (P125) MAY BE A BIFUNCTIONAL PROTEIN
CC WITH HELICASE AND PROTEASE ACTIVITY.
CC -!- PTM: GP116 GIVES RISE TO GP62 AND GP53; GP62 IN TURN YIELDS GP48
CC AND GP25.
CC -!- SIMILARITY: TO THE HOG CHOLERA VIRUS GENOME POLYPROTEIN.
CC -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S31.
DR EMBL; M96751; G289508; -.
DR PIR; A44217; A44217.
DR PROSITE; PS00531; RNASE T2 2.
KW POLYPROTEIN; GLYCOPROTEIN; HELICASE; SERINE PROTEASE; HYDROLASE.

FT	CHAIN	1	2270	P20 (30KD).
FT	CHAIN	2271	21063	GP116/GP62-GP53 (GLYCOPROTEIN).
FT	CHAIN	?	?	GP125/GP54-GP80.
FT	CHAIN	?	3898	GP133/GP58-GP75.
FT	DOMAIN	690	755	CYS-RICH.
FT	ACT_SITE	1658	1658	CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	ACT_SITE	1695	1695	CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	ACT_SITE	1752	1752	CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	CARBOHYD	272	272	POTENTIAL.
FT	CARBOHYD	281	281	POTENTIAL.
FT	CARBOHYD	296	296	POTENTIAL.
FT	CARBOHYD	335	335	POTENTIAL.
FT	CARBOHYD	365	365	POTENTIAL.
FT	CARBOHYD	370	370	POTENTIAL.
FT	CARBOHYD	413	413	POTENTIAL.
FT	CARBOHYD	487	487	POTENTIAL.
FT	CARBOHYD	597	597	POTENTIAL.
FT	CARBOHYD	809	809	POTENTIAL.
FT	CARBOHYD	878	878	POTENTIAL.
FT	CARBOHYD	922	922	POTENTIAL.
FT	CARBOHYD	990	990	POTENTIAL.
FT	CARBOHYD	1357	1357	POTENTIAL.
FT	CARBOHYD	1419	1419	POTENTIAL.
FT	CARBOHYD	1451	1451	POTENTIAL.
FT	CARBOHYD	1713	1713	POTENTIAL.
FT	CARBOHYD	2134	2134	POTENTIAL.
FT	CARBOHYD	2217	2217	POTENTIAL.
FT	CARBOHYD	2494	2494	POTENTIAL.
FT	CARBOHYD	2682	2682	POTENTIAL.
FT	CARBOHYD	2751	2751	POTENTIAL.
FT	CARBOHYD	2891	2891	POTENTIAL.
FT	CARBOHYD	2988	2988	POTENTIAL.
FT	CARBOHYD	3688	3688	POTENTIAL.
FT	CARBOHYD	3777	3777	POTENTIAL.
FT	CARBOHYD	3793	3793	POTENTIAL.
FT	SEQUENCE	3898 AA;	437800 MW;	A562145C CRC32;
Seq Match			60.5%;	Score 49; DB 7; Length 3898;
Best Local Similarity			58.3%;	Pred. No. 9.49e-01;
Matches		7;	Conservative	2; Mismatches 3; Indels 0; Gaps 0;
Db	1132	dtvkdpgggggy	1143	
QV	1	DVKADPTGHSY	12	

Search completed: Thu Apr 3 11:59:16 1997
Job time : 6 secs.